

SEQUENCE LISTING

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Zelder, Oskar
Kolpprogge, Corinna
Schroder, Hartwig
Hafner, Stefan

<120> Method for Production by Fermentation of Sulphur-Containing Fine
Chemicals (metF)

<130> 13111-00005-US

<150> PCT/EP 2003/009451

<151> 2003-08-26

<150> DE 102 39 308.7

<151> 2002-08-27

<160> 77

<170> PatentIn version 3.3

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<212> DNA

<213> corynebacterium diphteriae

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<222> (1)..(981)

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acc	caa	gaa	gaa	tta	gaa	gaa	att	ctg	tgc	act	tat	gcg	tcc	cac	ggg	336
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Pro	Gly	Leu	Met	Pro	Ile	Thr	Ser	Leu	Arg	Ser	Val	Arg	Arg	Gln	Met		
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<213> corynebacterium diphteriae

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Asp Arg Leu Val Lys Ala Asp Pro Glu His Gly Ser Lys Pro Ile Ile
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Val Gly Ile Glu Val Thr Thr Glu Met Ala Gln Arg Leu Ile Ser Glu
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gcc gac acc acg ctg acc ccg gtg gcc cac ctc acc gcc gtc gac cac 288
 Ala Asp Thr Thr Leu Thr Pro Val Ala His Leu Thr Ala Val Asp His
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tcc gtc gcc gag ctg cgc aac atc atc ggc cag tac gcc gac gcc ggg 336
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 Pro Ala Glu Leu Lys Glu Arg Ile Leu Thr Ala Lys Asp Asp Pro Ala
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gct gta cgc tcg atc ggc atc gag ttc gcc acg gag ttc tgc gcg cgg 816
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ctg ctg gcc gag gga gtg cca gga ctg cac ttc atc acg ctc aac aac 864
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 275 280 285

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 Ile Arg Asn Met Leu Ala Val Arg Gly Asp Pro Pro Gly Asp Pro Asn
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 145 150 155 160
 Phe Pro Glu Met His Pro Arg Ser Ala Asp Trp Asp Thr Asp Val Thr
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 Asn Phe Val Asp Lys Cys Arg Ala Gly Ala Asp Tyr Ala Ile Thr Gln
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 195 200 205
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 Ser Val Lys Met Leu Glu Arg Leu Pro Lys Leu Ser Asn Ala Ser Phe
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 260 265 270
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gcg ccg aag acg ccc aag ggc gag agg aac ctc tgg agc gcg ctg cgg	144
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Ser Val Ala Glu Leu Arg Asn Ile Ile Gly Gln Tyr Ala Asp Ala Gly	
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Asn Phe Val Asp Lys Cys Arg Ala Gly Ala Asp Tyr Ala Ile Thr Gln	
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 245 250 255

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 260 265 270

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Gly Gly Ser Thr Arg Ala Gly Thr Val Arg Glu Thr Gln Gln Ile Val
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Ser Val Ala Glu Leu Arg Asn Ile Ile Gly Gln Tyr Ala Asp Ala Gly
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Ile Arg Asn Met Leu Ala Val Arg Gly Asp Pro Pro Gly Asp Pro Asn
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Ala Asp Trp Ile Ala His Pro Glu Gly Leu Thr Tyr Ala Ala Glu Leu
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Phe Pro Glu Met His Pro Arg Ser Ala Asp Trp Asp Thr Asp Val Thr
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Asn Phe Val Asp Lys Cys Arg Ala Gly Ala Asp Tyr Ala Ile Thr Gln
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Met Phe Phe Gln Pro Asp Ser Tyr Leu Arg Leu Arg Asp Arg Val Ala
195 200 205

Ala Ala Gly Cys Ala Thr Pro Val Ile Pro Glu Val Met Pro Val Thr
210 215 220

Ser Val Lys Met Leu Glu Arg Leu Pro Lys Leu Ser Asn Ala Ser Phe
225 230 235 240

Pro Ala Glu Leu Lys Glu Arg Ile Leu Thr Ala Lys Asp Asp Pro Ala
245 250 255

Ala Val Arg Ser Ile Gly Ile Glu Phe Ala Thr Glu Phe Cys Ala Arg
260 265 270

Leu Leu Ala Glu Gly Val Pro Gly Leu His Phe Ile Thr Leu Asn Asn
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act ata agg aaa ctt gag aaa tta aat cct act ttt gta tcc gtt act 144
Thr Ile Arg Lys Leu Glu Lys Leu Asn Pro Thr Phe Val Ser Val Thr
35 40 45

tac ggg gca ggt ggt tcg act aga gat aga act agg aat ata gta cag 192
Tyr Gly Ala Gly Gly Ser Thr Arg Asp Arg Thr Arg Asn Ile Val Gln
50 55 60

aaa ata cac gag gaa act aac ctc acc gtt atg gca cac ctc acc tgt 240
Lys Ile His Glu Glu Thr Asn Leu Thr Val Met Ala His Leu Thr Cys
65 70 75 80

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Ile Ala His Thr Arg Glu Glu Leu Ile Asp Ile Leu Gln Asp Tyr Lys	
85 90 95	
aac ata ggt ata gag aac att ctc gct ttg agg ggg gac gtt ccg agg	336
Asn Ile Gly Ile Glu Asn Ile Leu Ala Leu Arg Gly Asp Val Pro Arg	
100 105 110	
gac aaa ccg gac tgg aga ccg ccg aag ggt gcg tgc aag tat gca aaa	384
Asp Lys Pro Asp Trp Arg Pro Pro Lys Gly Ala Cys Lys Tyr Ala Lys	
115 120 125	
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Glu Leu Val Glu Leu Ile Arg Lys Glu Phe Gly Asp Trp Phe Ser Ile	
130 135 140	
gga gtg gct tct tat cct gaa gga cat ccg gaa tca ccg aac ctc gag	480
Gly Val Ala Ser Tyr Pro Glu Gly His Pro Glu Ser Pro Asn Leu Glu	
145 150 155 160	
tgg gaa gtg aag tac ttt aag gaa aag gta gag gca ggt gca gac ttc	528
Trp Glu Val Lys Tyr Phe Lys Glu Lys Val Glu Ala Gly Ala Asp Phe	
165 170 175	
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Ser Ile Thr Gln Met Phe Phe Val Asn Asp Tyr Tyr Tyr Arg Phe Val	
180 185 190	
gaa atg tgc aaa aat gca ggg ata gat ata tct ata att ccg gga att	624
Glu Met Cys Lys Asn Ala Gly Ile Asp Ile Ser Ile Ile Pro Gly Ile	
195 200 205	
atg cct att act aac ttc aaa cag ata aga aag ttt gct tct ctt tgc	672
Met Pro Ile Thr Asn Phe Lys Gln Ile Arg Lys Phe Ala Ser Leu Cys	
210 215 220	
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Gln Cys Leu Asp Leu Ile Glu His Gly Val Pro Gly Leu His Phe Tyr	
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      35             40             45

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Ser Ile Thr Gln Met Phe Phe Val Asn Asp Tyr Tyr Tyr Arg Phe Val
      180             185             190

Glu Met Cys Lys Asn Ala Gly Ile Asp Ile Ser Ile Ile Pro Gly Ile
      195             200             205

Met Pro Ile Thr Asn Phe Lys Gln Ile Arg Lys Phe Ala Ser Leu Cys
      210             215             220

Gly Ala Thr Ile Pro Gln Ser Leu Ile Glu Lys Leu Glu Lys Val Glu
      225             230             235             240

Asp Lys Pro Glu Glu Val Lys Lys Ile Gly Ile Glu Phe Ala Ile Asn
      245             250             255

Gln Cys Leu Asp Leu Ile Glu His Gly Val Pro Gly Leu His Phe Tyr
      260             265             270

Thr Leu Asn Lys Ser Asp Ala Thr Leu Lys Ile Tyr Glu Ala Ile Lys
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Asp Lys Ile Pro Ala Arg Ser Thr
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 <223> RBU14992

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 gaa ggc gtg gac aag ctg cgc gcc acg cgc gcc cag ctc gcc acg ctc 96
 Glu Gly Val Asp Lys Leu Arg Ala Thr Arg Ala Gln Leu Ala Thr Leu
 20 25 30
 aag ccc aag ttc gtg tcc gtc acg ttc ggc gcc ggc ggc tcg acg caa 144
 Lys Pro Lys Phe Val Ser Val Thr Phe Gly Ala Gly Gly Ser Thr Gln
 35 40 45
 cag ggc acg ctc gac acc gtc gtc gat atg gcg aag gaa ggg ctc gaa 192
 Gln Gly Thr Leu Asp Thr Val Val Asp Met Ala Lys Glu Gly Leu Glu
 50 55 60
 gcg gcg ccg cac gtg tcg tgc atc ggc tcg tcg aaa gag agc ctg cgc 240
 Ala Ala Pro His Val Ser Cys Ile Gly Ser Ser Lys Glu Ser Leu Arg
 65 70 75 80
 gcc att ctc aac gag tac cgc gca cat ggc atc cgc cat atc gtc gcg 288
 Ala Ile Leu Asn Glu Tyr Arg Ala His Gly Ile Arg His Ile Val Ala
 85 90 95
 ctg cgc ggc gat ctg ccg tcc ggc atg ggc gaa gtc ggc gag ctg cgc 336
 Leu Arg Gly Asp Leu Pro Ser Gly Met Gly Glu Val Gly Glu Leu Arg
 100 105 110
 tat gcg tcg gaa ctg gtg agc ttt atc cgc gcc gaa ttc ggc gac tgg 384
 Tyr Ala Ser Glu Leu Val Ser Phe Ile Arg Ala Glu Phe Gly Asp Trp
 115 120 125
 ttc tgc atc gag gtg gcc ggc tat ccg gaa tac cac ccg cag tcg cgc 432
 Phe Cys Ile Glu Val Ala Gly Tyr Pro Glu Tyr His Pro Gln Ser Arg
 130 135 140
 tcg ccg cgt cag gat ctg gaa aac ttc gcc cgc aag gtg aag gcc ggc 480
 Ser Pro Arg Gln Asp Leu Glu Asn Phe Ala Arg Lys Val Lys Ala Gly
 145 150 155 160
 gcc aat tcg gcg atc aca cag tac ttc ttc aat gca gac gcg tat ttc 528
 Ala Asn Ser Ala Ile Thr Gln Tyr Phe Phe Asn Ala Asp Ala Tyr Phe
 165 170 175
 cgt ttc gtc gac gac gcg aga aag ctc ggc gtg gac gtg ccg atc gtg 576
 Arg Phe Val Asp Asp Ala Arg Lys Leu Gly Val Asp Val Pro Ile Val

180	185	190	
ccg ggc atc atg ccg atc acg aac ttc tcg cag ctg atg cgt ttc tcg			624
Pro Gly Ile Met Pro Ile Thr Asn Phe Ser Gln Leu Met Arg Phe Ser			
195	200	205	
gag atg tgc ggc gct gaa gtg cca cgc tgg atc gcg cgc cgg ctg gaa			672
Glu Met Cys Gly Ala Glu Val Pro Arg Trp Ile Ala Arg Arg Leu Glu			
210	215	220	
agc ttc ggc gac gat cgc gag tca att cgc gcg ttc ggg ctg gat gtg			720
Ser Phe Gly Asp Asp Arg Glu Ser Ile Arg Ala Phe Gly Leu Asp Val			
225	230	235	240
gtg acg gac ctg tgc agg cgt ctg atc gat gcg aag gtg ccg ggc ctg			768
Val Thr Asp Leu Cys Arg Arg Leu Ile Asp Ala Lys Val Pro Gly Leu			
245	250	255	
cac ttc tac acg cta aac ggc gca gcg gcg acc aag gcg atc tgc gaa			816
His Phe Tyr Thr Leu Asn Gly Ala Ala Thr Lys Ala Ile Cys Glu			
260	265	270	
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Arg Leu Asn Val			
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 <213> Burkholderia cepacia

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 35 40 45
 Gln Gly Thr Leu Asp Thr Val Val Asp Met Ala Lys Glu Gly Leu Glu
 50 55 60
 Ala Ala Pro His Val Ser Cys Ile Gly Ser Ser Lys Glu Ser Leu Arg
 65 70 75 80
 Ala Ile Leu Asn Glu Tyr Arg Ala His Gly Ile Arg His Ile Val Ala
 85 90 95
 Leu Arg Gly Asp Leu Pro Ser Gly Met Gly Glu Val Gly Glu Leu Arg
 100 105 110
 Tyr Ala Ser Glu Leu Val Ser Phe Ile Arg Ala Glu Phe Gly Asp Trp
 115 120 125
 Phe Cys Ile Glu Val Ala Gly Tyr Pro Glu Tyr His Pro Gln Ser Arg
 130 135 140

Ser Pro Arg Gln Asp Leu Glu Asn Phe Ala Arg Lys Val Lys Ala Gly
 145 150 155 160
 Ala Asn Ser Ala Ile Thr Gln Tyr Phe Phe Asn Ala Asp Ala Tyr Phe
 165 170 175
 Arg Phe Val Asp Asp Ala Arg Lys Leu Gly Val Asp Val Pro Ile Val
 180 185 190
 Pro Gly Ile Met Pro Ile Thr Asn Phe Ser Gln Leu Met Arg Phe Ser
 195 200 205
 Glu Met Cys Gly Ala Glu Val Pro Arg Trp Ile Ala Arg Arg Leu Glu
 210 215 220
 Ser Phe Gly Asp Asp Arg Glu Ser Ile Arg Ala Phe Gly Leu Asp Val
 225 230 235 240
 Val Thr Asp Leu Cys Arg Arg Leu Ile Asp Ala Lys Val Pro Gly Leu
 245 250 255
 His Phe Tyr Thr Leu Asn Gly Ala Ala Ala Thr Lys Ala Ile Cys Glu
 260 265 270
 Arg Leu Asn Val
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 <212> DNA
 <213> Nitrosomonas europaea

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 <223> RNE02657

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 Pro Pro Gln Thr Pro Glu Gly Met Glu Lys Leu Arg Ala Thr Arg Ile
 20 25 30
 cag ctt gct cag ttc aat ccg aag ttt ttt tcg gtg acg ttt ggt gcc 144
 Gln Leu Ala Gln Phe Asn Pro Lys Phe Phe Ser Val Thr Phe Gly Ala
 35 40 45
 ggc gga tcc act cgt gaa cgc acg ctc gaa acc gtg ctg gaa att cag 192
 Gly Gly Ser Thr Arg Glu Arg Thr Leu Glu Thr Val Leu Glu Ile Gln
 50 55 60
 gca gaa ggc tat ccg gta gcg ccc cat ctt tcc tgt atc ggc tcc acg 240
 Ala Glu Gly Tyr Pro Val Ala Pro His Leu Ser Cys Ile Gly Ser Thr
 65 70 75 80

cgt gac aat atc cgt tgc atc ctt gag aaa tat cac agt cac ggt atc	288
Arg Asp Asn Ile Arg Ser Ile Leu Glu Lys Tyr His Ser His Gly Ile	
85 90 95	
agc cgc att gtg gcg cta cgt ggt gat tta ccc tcc ggc atg gcg cag	336
Ser Arg Ile Val Ala Leu Arg Gly Asp Leu Pro Ser Gly Met Ala Gln	
100 105 110	
gcg gga gaa ttc cgc tac gcc aac gag ctg gta gca ttt atc cgc aag	384
Ala Gly Glu Phe Arg Tyr Ala Asn Glu Leu Val Ala Phe Ile Arg Lys	
115 120 125	
gag ttc ggt gat acc ttc tgg atc gaa gtg gcg gct tat ccg gaa tat	432
Glu Phe Gly Asp Thr Phe Trp Ile Glu Val Ala Ala Tyr Pro Glu Tyr	
130 135 140	
cat cca caa gcc cgc tcc gct ctg gag gat ttc acc aat ttc aga cga	480
His Pro Gln Ala Arg Ser Ala Leu Glu Asp Phe Thr Asn Phe Arg Arg	
145 150 155 160	
aaa gtc gaa gca ggt tcc aat gca gcg att acc cag ttt ttc tat aac	528
Lys Val Glu Ala Gly Ser Asn Ala Ala Ile Thr Gln Phe Phe Tyr Asn	
165 170 175	
gtg gat gcc tat ctg cat ttc gta gag atg tgt gaa gct gcg gat ctg	576
Val Asp Ala Tyr Leu His Phe Val Glu Met Cys Glu Ala Ala Asp Leu	
180 185 190	
aat atc ccg atc gtt ccc ggc atc atg ccg atc agc aaa ttt tct caa	624
Asn Ile Pro Ile Val Pro Gly Ile Met Pro Ile Ser Lys Phe Ser Gln	
195 200 205	
ctg gca aga ttt tgc gat ggc tgt gga gca gaa att cca cgc tgg att	672
Leu Ala Arg Phe Ser Asp Gly Cys Gly Ala Glu Ile Pro Arg Trp Ile	
210 215 220	
cgc aga aaa ctg gaa agc ttc ggt gat gat att ccg tct atc cag gca	720
Arg Arg Lys Leu Glu Ser Phe Gly Asp Asp Ile Pro Ser Ile Gln Ala	
225 230 235 240	
ttc ggg ctg gat gtc gtc aca gcg tta tgt gct cgt ctg ctg gaa gcc	768
Phe Gly Leu Asp Val Val Thr Ala Leu Cys Ala Arg Leu Leu Glu Ala	
245 250 255	
ggc gca ccc ggc ctg cat ttc tac aca ctc aac tcc gcc gta cta ccc	816
Gly Ala Pro Gly Leu His Phe Tyr Thr Leu Asn Ser Ala Val Leu Pro	
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aca aaa atc tgg caa cgc ctg ggg tta tag	846
Thr Lys Ile Trp Gln Arg Leu Gly Leu	
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<212> PRT

<213> Nitrosomonas europaea

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 35 40 45
 Gly Gly Ser Thr Arg Glu Arg Thr Leu Glu Thr Val Leu Glu Ile Gln
 50 55 60
 Ala Glu Gly Tyr Pro Val Ala Pro His Leu Ser Cys Ile Gly Ser Thr
 65 70 75 80
 Arg Asp Asn Ile Arg Ser Ile Leu Glu Lys Tyr His Ser His Gly Ile
 85 90 95
 Ser Arg Ile Val Ala Leu Arg Gly Asp Leu Pro Ser Gly Met Ala Gln
 100 105 110
 Ala Gly Glu Phe Arg Tyr Ala Asn Glu Leu Val Ala Phe Ile Arg Lys
 115 120 125
 Glu Phe Gly Asp Thr Phe Trp Ile Glu Val Ala Ala Tyr Pro Glu Tyr
 130 135 140
 His Pro Gln Ala Arg Ser Ala Leu Glu Asp Phe Thr Asn Phe Arg Arg
 145 150 155 160
 Lys Val Glu Ala Gly Ser Asn Ala Ala Ile Thr Gln Phe Phe Tyr Asn
 165 170 175
 Val Asp Ala Tyr Leu His Phe Val Glu Met Cys Glu Ala Ala Asp Leu
 180 185 190
 Asn Ile Pro Ile Val Pro Gly Ile Met Pro Ile Ser Lys Phe Ser Gln
 195 200 205
 Leu Ala Arg Phe Ser Asp Gly Cys Gly Ala Glu Ile Pro Arg Trp Ile
 210 215 220
 Arg Arg Lys Leu Glu Ser Phe Gly Asp Asp Ile Pro Ser Ile Gln Ala
 225 230 235 240
 Phe Gly Leu Asp Val Val Thr Ala Leu Cys Ala Arg Leu Leu Glu Ala
 245 250 255
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 260 265 270
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<210> 13

<211> 873

<212> DNA

<213> *Pseudomonas aeruginosa*

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<222> (1)..(870)

<223> RPA03308

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Ser Phe Glu Phe Phe Pro Ala Lys Thr Glu Ala Gly His Glu Lys Leu	
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Leu Ala Thr Ala Arg Asn Leu Ala Gly Tyr Lys Pro Asp Phe Phe Ser	
35 40 45	
tgc acc tac ggc gcc ggc gga tcc acc cgc gac cgc acg ttg agt acc	192
Cys Thr Tyr Gly Ala Gly Gly Ser Thr Arg Asp Arg Thr Leu Ser Thr	
50 55 60	
gtg ctg caa ctg gac ggc gag gtg aag gtg ccg acc gcg ccg cac ctg	240
Val Leu Gln Leu Asp Gly Glu Val Lys Val Pro Thr Ala Pro His Leu	
65 70 75 80	
tcc tgt gtc ggc gac tcg aaa gcc gag ttg cgc gaa ctg ctc ggc cgc	288
Ser Cys Val Gly Asp Ser Lys Ala Glu Leu Arg Glu Leu Leu Gly Arg	
85 90 95	
tac cgc gag gcc ggc atc cgc cgc atc gtc gcc ctg cgc ggc gac ctg	336
Tyr Arg Glu Ala Gly Ile Arg Arg Ile Val Ala Leu Arg Gly Asp Leu	
100 105 110	
ccg tcg ggc atg ggc atg gcc agc ggc gaa ctg cgc tac gcc aac gaa	384
Pro Ser Gly Met Gly Met Ala Ser Gly Glu Leu Arg Tyr Ala Asn Glu	
115 120 125	
ctg gtg gac ttc atc cgc acc gag acc ggc gac cac ttc cac atc gag	432
Leu Val Asp Phe Ile Arg Thr Glu Thr Gly Asp His Phe His Ile Glu	
130 135 140	
gtc gcc gcc tat ccg gag gtc cac ccc cag gcg cgc agc ttc gag gat	480
Val Ala Ala Tyr Pro Glu Val His Pro Gln Ala Arg Ser Phe Glu Asp	
145 150 155 160	
gac ctg gcg aac ttc gtg cgc aag gtg aag gcc ggc gcc agc agc gcc	528
Asp Leu Ala Asn Phe Val Arg Lys Val Lys Ala Gly Ala Ser Ser Ala	
165 170 175	
atc acc cag tac ttc ttc aac gcc gat gcc tat ttc tac ttc gtc gag	576
Ile Thr Gln Tyr Phe Phe Asn Ala Asp Ala Tyr Phe Tyr Phe Val Glu	
180 185 190	
cgg gtc gcc aag ctg ggc gtg gac atc ccg gtg gtc ccc ggc atc atg	624
Arg Val Ala Lys Leu Gly Val Asp Ile Pro Val Val Pro Gly Ile Met	
195 200 205	
ccg atc acc aac tac tcc aag ctg gcg cgc ttc tcc gac gcc tgc ggc	672

Pro Ile Thr Asn Tyr Ser Lys Leu Ala Arg Phe Ser Asp Ala Cys Gly
 210 215 220

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 225 230 235 240

gac agc cgc agc atc cag gcc ttc ggc gag cag gtc atc agc gag atg 768
 Asp Ser Arg Ser Ile Gln Ala Phe Gly Glu Gln Val Ile Ser Glu Met
 245 250 255

tgc gaa cgc ctg ctg gag ggc ggc gca ccg gga ctg cat ttc tat act 816
 Cys Glu Arg Leu Leu Glu Gly Gly Ala Pro Gly Leu His Phe Tyr Thr
 260 265 270

ttg aac cag gcc gat ccg agc ctg gcg atc tgg aag aat ctc cag ctg 864
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 Pro Arg
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 <213> Pseudomonas aeruginosa

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 35 40 45

Cys Thr Tyr Gly Ala Gly Gly Ser Thr Arg Asp Arg Thr Leu Ser Thr
 50 55 60

Val Leu Gln Leu Asp Gly Glu Val Lys Val Pro Thr Ala Pro His Leu
 65 70 75 80

Ser Cys Val Gly Asp Ser Lys Ala Glu Leu Arg Glu Leu Leu Gly Arg
 85 90 95

Tyr Arg Glu Ala Gly Ile Arg Arg Ile Val Ala Leu Arg Gly Asp Leu
 100 105 110

Pro Ser Gly Met Gly Met Ala Ser Gly Glu Leu Arg Tyr Ala Asn Glu
 115 120 125

Leu Val Asp Phe Ile Arg Thr Glu Thr Gly Asp His Phe His Ile Glu
 130 135 140

Val Ala Ala Tyr Pro Glu Val His Pro Gln Ala Arg Ser Phe Glu Asp
 145 150 155 160

Asp Leu Ala Asn Phe Val Arg Lys Val Lys Ala Gly Ala Ser Ser Ala
 165 170 175

Ile Thr Gln Tyr Phe Phe Asn Ala Asp Ala Tyr Phe Tyr Phe Val Glu
 180 185 190

Arg Val Ala Lys Leu Gly Val Asp Ile Pro Val Val Pro Gly Ile Met
 195 200 205

Pro Ile Thr Asn Tyr Ser Lys Leu Ala Arg Phe Ser Asp Ala Cys Gly
 210 215 220

Ala Glu Leu Pro Arg Trp Ile Arg Lys Gln Leu Glu Ala Tyr Gly Asp
 225 230 235 240

Asp Ser Arg Ser Ile Gln Ala Phe Gly Glu Gln Val Ile Ser Glu Met
 245 250 255

Cys Glu Arg Leu Leu Glu Gly Gly Ala Pro Gly Leu His Phe Tyr Thr
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 275 280 285

Pro Arg
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 <223> RXFX00359

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 gaa tac gtc tcc tgc acc ttc ggc gcc ggt ggc tcc aca ctc agt tac 144
 Glu Tyr Val Ser Cys Thr Phe Gly Ala Gly Gly Ser Thr Leu Ser Tyr
 35 40 45
 acc tca gaa aca gtg cgc cat ctc agc caa cac cac ggc ttt gac gcc 192
 Thr Ser Glu Thr Val Arg His Leu Ser Gln His His Gly Phe Asp Ala
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 Ala Pro His Leu Ser Cys Val Gly Gly Ser Arg Gln Glu Ile Arg Glu
 65 70 75 80

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Leu Leu Lys Leu Tyr Arg Ala Ile Gly Cys Gln Arg Ile Val Ala Leu	
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Arg Gly Asp Leu Pro Ser Gly Met Gly His Pro Gly Asp Leu Arg Tyr	
100 105 110	
gca gct gac ctg att acc ttc atc cgt acc gag cat ggc gat cac ttc	384
Ala Ala Asp Leu Ile Thr Phe Ile Arg Thr Glu His Gly Asp His Phe	
115 120 125	
cac cta gag atc ggc gca tac ccg gaa acc cac cca caa gcc agc aac	432
His Leu Glu Ile Gly Ala Tyr Pro Glu Thr His Pro Gln Ala Ser Asn	
130 135 140	
aca ctg aac gac ctt cac tat ttc aaa gcc aaa gcc gat gca ggc gcc	480
Thr Leu Asn Asp Leu His Tyr Phe Lys Ala Lys Ala Asp Ala Gly Ala	
145 150 155 160	
gat gcg gca atc act caa tac ttt tat aac cca gac gcc tat ttc cac	528
Asp Ala Ala Ile Thr Gln Tyr Phe Tyr Asn Pro Asp Ala Tyr Phe His	
165 170 175	
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Phe Val Asp Ala Val Gln Arg Leu Gly Val Thr Ile Pro Ile Val Ala	
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Gly Val Met Pro Ile Ser Asn Phe Asp Gln Leu Arg His Phe Ser Glu	
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Gln Cys Gly Ala Glu Ile Pro Arg Trp Ile Thr Lys Lys Met Gln Ala	
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Tyr Gly Asp Asp Thr Lys Ser Ile Arg Ala Phe Gly Ala Asp Val Val	
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Thr Ala Leu Cys Glu Arg Leu Ile Ala Gly Gly Ala Pro Gly Leu His	
245 250 255	
ttc tac acg ctc aac cta gcc aaa cca agc acc caa gtg ctg caa cgc	816
Phe Tyr Thr Leu Asn Leu Ala Lys Pro Ser Thr Gln Val Leu Gln Arg	
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Leu Gly Tyr	
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<210> 16

<211> 275

<212> PRT

<213> Xylella almond

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 35 40 45
 Thr Ser Glu Thr Val Arg His Leu Ser Gln His His Gly Phe Asp Ala
 50 55 60
 Ala Pro His Leu Ser Cys Val Gly Gly Ser Arg Gln Glu Ile Arg Glu
 65 70 75 80
 Leu Leu Lys Leu Tyr Arg Ala Ile Gly Cys Gln Arg Ile Val Ala Leu
 85 90 95
 Arg Gly Asp Leu Pro Ser Gly Met Gly His Pro Gly Asp Leu Arg Tyr
 100 105 110
 Ala Ala Asp Leu Ile Thr Phe Ile Arg Thr Glu His Gly Asp His Phe
 115 120 125
 His Leu Glu Ile Gly Ala Tyr Pro Glu Thr His Pro Gln Ala Ser Asn
 130 135 140
 Thr Leu Asn Asp Leu His Tyr Phe Lys Ala Lys Ala Asp Ala Gly Ala
 145 150 155 160
 Asp Ala Ala Ile Thr Gln Tyr Phe Tyr Asn Pro Asp Ala Tyr Phe His
 165 170 175
 Phe Val Asp Ala Val Gln Arg Leu Gly Val Thr Ile Pro Ile Val Ala
 180 185 190
 Gly Val Met Pro Ile Ser Asn Phe Asp Gln Leu Arg His Phe Ser Glu
 195 200 205
 Gln Cys Gly Ala Glu Ile Pro Arg Trp Ile Thr Lys Lys Met Gln Ala
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 Tyr Gly Asp Asp Thr Lys Ser Ile Arg Ala Phe Gly Ala Asp Val Val
 225 230 235 240
 Thr Ala Leu Cys Glu Arg Leu Ile Ala Gly Gly Ala Pro Gly Leu His
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<211> 828

<212> DNA

<213> Xylella oleander

<220>

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<222> (1)..(825)

<223> RXYF01676

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Glu Tyr Val Ser Cys Thr Phe Gly Ala Gly Gly Ser Thr Leu Ser Tyr	
35 40 45	
acc tca gaa aca gtg cgc cat ctc agt caa cac cac ggc ttt gac acc	192
Thr Ser Glu Thr Val Arg His Leu Ser Gln His His Gly Phe Asp Thr	
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gca ccg cat ctg tcc tgt gtg ggc ggc agt cgc caa gaa atc cgc gaa	240
Ala Pro His Leu Ser Cys Val Gly Gly Ser Arg Gln Glu Ile Arg Glu	
65 70 75 80	
ctt ctc aaa ctg tac cgc gcg att ggc tgc caa cgc atc gtg gcg cta	288
Leu Leu Lys Leu Tyr Arg Ala Ile Gly Cys Gln Arg Ile Val Ala Leu	
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cgc ggc gat ctc ccc tcg ggc atg ggc cac ccc ggc gac ctc cgc tac	336
Arg Gly Asp Leu Pro Ser Gly Met Gly His Pro Gly Asp Leu Arg Tyr	
100 105 110	
gca gct gac ctg att acc ttc atc cgt gcc gag cat ggc gat cac ttc	384
Ala Ala Asp Leu Ile Thr Phe Ile Arg Ala Glu His Gly Asp His Phe	
115 120 125	
cac cta gag atc ggc gca tac ccg gaa acc cac cca caa gcc agc aac	432
His Leu Glu Ile Gly Ala Tyr Pro Glu Thr His Pro Gln Ala Ser Asn	
130 135 140	
aca ctg aac gac ctt cac tat ttc aaa gcc aaa gcc gat gca ggc gcc	480
Thr Leu Asn Asp Leu His Tyr Phe Lys Ala Lys Ala Asp Ala Gly Ala	
145 150 155 160	
gat gcg gca atc act caa tac ttt tac aac cca gac gcc tat ttc cac	528
Asp Ala Ala Ile Thr Gln Tyr Phe Tyr Asn Pro Asp Ala Tyr Phe His	
165 170 175	
ttc gtc gac gca gtg cag cgc ctg ggc gtc acc atc ccc att gtt gcc	576
Phe Val Asp Ala Val Gln Arg Leu Gly Val Thr Ile Pro Ile Val Ala	
180 185 190	
gga gtc atg ccc atc tcc aac ttt gac cag ttg cgc cat ttc tcc gaa	624
Gly Val Met Pro Ile Ser Asn Phe Asp Gln Leu Arg His Phe Ser Glu	
195 200 205	

caa tgc ggc gcc gaa ata ccc cgc tgg att aca aaa aaa atg cag gct 672
 Gln Cys Gly Ala Glu Ile Pro Arg Trp Ile Thr Lys Lys Met Gln Ala
 210 215 220

tac ggc gat gac acc aaa tcg ata cgc gcg ttc ggt gcc gac gtc gtg 720
 Tyr Gly Asp Asp Thr Lys Ser Ile Arg Ala Phe Gly Ala Asp Val Val
 225 230 235 240

acc gca cta tgt gag cgg cta atc gct ggc ggc gca ccg ggg ctg cac 768
 Thr Ala Leu Cys Glu Arg Leu Ile Ala Gly Gly Ala Pro Gly Leu His
 245 250 255

ttc tac acg ctc aac cta gcc aaa cca agc acc caa gtg ctg caa cgc 816
 Phe Tyr Thr Leu Asn Leu Ala Lys Pro Ser Thr Gln Val Leu Gln Arg
 260 265 270

tta ggc tat tga 828
 Leu Gly Tyr
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 <212> PRT
 <213> Xylella oleander

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Arg Ala Gln Leu Asp Arg Thr Ala Asn Arg Leu Arg Ala Phe Ala Pro
 20 25 30

Glu Tyr Val Ser Cys Thr Phe Gly Ala Gly Gly Ser Thr Leu Ser Tyr
 35 40 45

Thr Ser Glu Thr Val Arg His Leu Ser Gln His His Gly Phe Asp Thr
 50 55 60

Ala Pro His Leu Ser Cys Val Gly Gly Ser Arg Gln Glu Ile Arg Glu
 65 70 75 80

Leu Leu Lys Leu Tyr Arg Ala Ile Gly Cys Gln Arg Ile Val Ala Leu
 85 90 95

Arg Gly Asp Leu Pro Ser Gly Met Gly His Pro Gly Asp Leu Arg Tyr
 100 105 110

Ala Ala Asp Leu Ile Thr Phe Ile Arg Ala Glu His Gly Asp His Phe
 115 120 125

His Leu Glu Ile Gly Ala Tyr Pro Glu Thr His Pro Gln Ala Ser Asn
 130 135 140

Thr Leu Asn Asp Leu His Tyr Phe Lys Ala Lys Ala Asp Ala Gly Ala
 145 150 155 160

Asp Ala Ala Ile Thr Gln Tyr Phe Tyr Asn Pro Asp Ala Tyr Phe His

165					170					175					
Phe	Val	Asp	Ala	Val	Gln	Arg	Leu	Gly	Val	Thr	Ile	Pro	Ile	Val	Ala
			180					185					190		
Gly	Val	Met	Pro	Ile	Ser	Asn	Phe	Asp	Gln	Leu	Arg	His	Phe	Ser	Glu
		195					200					205			
Gln	Cys	Gly	Ala	Glu	Ile	Pro	Arg	Trp	Ile	Thr	Lys	Lys	Met	Gln	Ala
		210					215					220			
Tyr	Gly	Asp	Asp	Thr	Lys	Ser	Ile	Arg	Ala	Phe	Gly	Ala	Asp	Val	Val
		225					230					235			240
Thr	Ala	Leu	Cys	Glu	Arg	Leu	Ile	Ala	Gly	Gly	Ala	Pro	Gly	Leu	His
			245						250					255	
Phe	Tyr	Thr	Leu	Asn	Leu	Ala	Lys	Pro	Ser	Thr	Gln	Val	Leu	Gln	Arg
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<210> 19

<211> 846

<212> DNA

<213> *Pseudomonas fluorescens*

<220>

<221> CDS

<222> (1)..(843)

<223> RPU04845

<400> 19

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Met	Ser	Gln	Asp	Arg	Arg	Tyr	Ser	Phe	Glu	Phe	Phe	Pro	Thr	Lys	Thr	
1				5					10					15		

gat	gct	ggg	cat	gaa	aaa	ctg	ctc	gcc	act	gcc	cgt	cag	ctg	gcc	acc	96
Asp	Ala	Gly	His	Glu	Lys	Leu	Leu	Ala	Thr	Ala	Arg	Gln	Leu	Ala	Thr	
			20					25					30			

tat	aag	cct	gac	ttc	ttt	tcc	tgc	acc	tac	ggc	gct	ggc	ggg	tgc	acc	144
Tyr	Lys	Pro	Asp	Phe	Phe	Ser	Cys	Thr	Tyr	Gly	Ala	Gly	Gly	Ser	Thr	
		35					40					45				

cgt	gac	cgc	acg	ctg	aac	acc	gtt	ctg	cag	ctg	gaa	agc	gaa	gtc	aaa	192
Arg	Asp	Arg	Thr	Leu	Asn	Thr	Val	Leu	Gln	Leu	Glu	Ser	Glu	Val	Lys	
		50				55					60					

atc	ccc	gcc	gca	ccg	cac	ctg	tcg	tgc	gtc	ggc	gac	agc	aag	gac	gac	240
Ile	Pro	Ala	Ala	Pro	His	Leu	Ser	Cys	Val	Gly	Asp	Ser	Lys	Asp	Asp	
		65			70				75					80		

ctg	cgc	ggc	ctg	ctg	aac	gag	tac	aag	gcc	gcc	ggc	atc	aag	cgc	atc	288
Leu	Arg	Gly	Leu	Leu	Asn	Glu	Tyr	Lys	Ala	Ala	Gly	Ile	Lys	Arg	Ile	
			85						90					95		

gtc gcc ctg cgc ggt gac ctg ccg tcc ggc atg ggc atg acc agc ggc 336
 Val Ala Leu Arg Gly Asp Leu Pro Ser Gly Met Gly Met Thr Ser Gly
 100 105 110

gag ctg cgt cac gcc aat gaa ctg gtt gaa ttc att cgt gaa gaa acc 384
 Glu Leu Arg His Ala Asn Glu Leu Val Glu Phe Ile Arg Glu Glu Thr
 115 120 125

ggc aat cat ttc cac atc gaa gtc gcc gcc tac ccg gag atg cat ccg 432
 Gly Asn His Phe His Ile Glu Val Ala Ala Tyr Pro Glu Met His Pro
 130 135 140

caa gcg cgc aac tac gaa gac gat ctc gcc aac ttc gtg cgc aag gcc 480
 Gln Ala Arg Asn Tyr Glu Asp Asp Leu Ala Asn Phe Val Arg Lys Ala
 145 150 155 160

cgt gcc ggc gcc gac agc gcg atc acc cag tac ttc ttc aac gcc gac 528
 Arg Ala Gly Ala Asp Ser Ala Ile Thr Gln Tyr Phe Phe Asn Ala Asp
 165 170 175

agc tac ttc tac ttc gtc gac cgt ttg cag gcg ctg ggc gtg gac att 576
 Ser Tyr Phe Tyr Phe Val Asp Arg Leu Gln Ala Leu Gly Val Asp Ile
 180 185 190

ccg gtg gta ccg ggg atc atg ccg atc acc aac tac agc aaa ctc gcg 624
 Pro Val Val Pro Gly Ile Met Pro Ile Thr Asn Tyr Ser Lys Leu Ala
 195 200 205

cgc ttc tcc gat gcc tgc ggt gcg gaa atc ccg cgc tgg atc cgc aag 672
 Arg Phe Ser Asp Ala Cys Gly Ala Glu Ile Pro Arg Trp Ile Arg Lys
 210 215 220

cag ctg gaa gcc tac ggc gat gac agc caa agc att cag cgc ttt ggc 720
 Gln Leu Glu Ala Tyr Gly Asp Asp Ser Gln Ser Ile Gln Arg Phe Gly
 225 230 235 240

gaa caa gtc gtc acg gaa atg tgc gaa cgc ctg ctg caa ggc ggc gcg 768
 Glu Gln Val Val Thr Glu Met Cys Glu Arg Leu Leu Gln Gly Gly Ala
 245 250 255

ccc ggc ctg cac ttc tat tcc atg aac cag gcc gaa cca agc ctg gcg 816
 Pro Gly Leu His Phe Tyr Ser Met Asn Gln Ala Glu Pro Ser Leu Ala
 260 265 270

atc tgg aac aac ctg aag ctg ccg cgc taa 846
 Ile Trp Asn Asn Leu Lys Leu Pro Arg
 275 280

<210> 20

<211> 281

<212> PRT

<213> *Pseudomonas fluorescens*

<400> 20

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Asp Ala Gly His Glu Lys Leu Leu Ala Thr Ala Arg Gln Leu Ala Thr
 20 25 30

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Tyr Lys Pro Asp Phe Phe Ser Cys Thr Tyr Gly Ala Gly Gly Ser Thr
    35                      40                      45

Arg Asp Arg Thr Leu Asn Thr Val Leu Gln Leu Glu Ser Glu Val Lys
    50                      55                      60

Ile Pro Ala Ala Pro His Leu Ser Cys Val Gly Asp Ser Lys Asp Asp
    65                      70                      75                      80

Leu Arg Gly Leu Leu Asn Glu Tyr Lys Ala Ala Gly Ile Lys Arg Ile
    85                      90                      95

Val Ala Leu Arg Gly Asp Leu Pro Ser Gly Met Gly Met Thr Ser Gly
    100                     105                     110

Glu Leu Arg His Ala Asn Glu Leu Val Glu Phe Ile Arg Glu Glu Thr
    115                     120                     125

Gly Asn His Phe His Ile Glu Val Ala Ala Tyr Pro Glu Met His Pro
    130                     135                     140

Gln Ala Arg Asn Tyr Glu Asp Asp Leu Ala Asn Phe Val Arg Lys Ala
    145                     150                     155                     160

Arg Ala Gly Ala Asp Ser Ala Ile Thr Gln Tyr Phe Phe Asn Ala Asp
    165                     170                     175

Ser Tyr Phe Tyr Phe Val Asp Arg Leu Gln Ala Leu Gly Val Asp Ile
    180                     185                     190

Pro Val Val Pro Gly Ile Met Pro Ile Thr Asn Tyr Ser Lys Leu Ala
    195                     200                     205

Arg Phe Ser Asp Ala Cys Gly Ala Glu Ile Pro Arg Trp Ile Arg Lys
    210                     215                     220

Gln Leu Glu Ala Tyr Gly Asp Asp Ser Gln Ser Ile Gln Arg Phe Gly
    225                     230                     235                     240

Glu Gln Val Val Thr Glu Met Cys Glu Arg Leu Leu Gln Gly Gly Ala
    245                     250                     255

Pro Gly Leu His Phe Tyr Ser Met Asn Gln Ala Glu Pro Ser Leu Ala
    260                     265                     270

Ile Trp Asn Asn Leu Lys Leu Pro Arg
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<210> 21

<211> 1812

<212> DNA

<213> Schizosaccharomyces pombe

<220>

<221> CDS

<222> (1) .. (1809)

<223> RSO01645

<400> 21

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act tac agt tat gaa ttt ttt cct cca aaa acg agc act ggt gtc caa	96
Thr Tyr Ser Tyr Glu Phe Phe Pro Pro Lys Thr Ser Thr Gly Val Gln	
20 25 30	
aat ctt tac aat cgt ata gat cgc atg aag act tgg ggt cgt ccc atg	144
Asn Leu Tyr Asn Arg Ile Asp Arg Met Lys Thr Trp Gly Arg Pro Met	
35 40 45	
ttt gtc gat gtg act tgg ggt gct ggt ggt act tct tca gaa ctg act	192
Phe Val Asp Val Thr Trp Gly Ala Gly Gly Thr Ser Ser Glu Leu Thr	
50 55 60	
cct gga atc gtt aat gta att caa aca gat ttt gaa gtg gat act tgc	240
Pro Gly Ile Val Asn Val Ile Gln Thr Asp Phe Glu Val Asp Thr Cys	
65 70 75 80	
atg cat ttg act tgt acg aac atg tcc aca gaa atg att gac gca gct	288
Met His Leu Thr Cys Thr Asn Met Ser Thr Glu Met Ile Asp Ala Ala	
85 90 95	
ttg aaa cgg gct cat gaa aca ggg tgt cgt aac ata ttg gcc ctt aga	336
Leu Lys Arg Ala His Glu Thr Gly Cys Arg Asn Ile Leu Ala Leu Arg	
100 105 110	
ggg gat cct gtt aaa gat aca gac tgg act gaa ggc gaa agt gga ttc	384
Gly Asp Pro Val Lys Asp Thr Asp Trp Thr Glu Gly Glu Ser Gly Phe	
115 120 125	
cgg tat gct tca gac tta gtt aga tat att cgc aca cat tat aat gat	432
Arg Tyr Ala Ser Asp Leu Val Arg Tyr Ile Arg Thr His Tyr Asn Asp	
130 135 140	
gaa ttc tgt att ggt gta gct ggc tat cca gaa gga tat tca cca gat	480
Glu Phe Cys Ile Gly Val Ala Gly Tyr Pro Glu Gly Tyr Ser Pro Asp	
145 150 155 160	
gat gac att gat gaa agc ata aag cat ctg aaa tta aaa gtc gat gaa	528
Asp Asp Ile Asp Glu Ser Ile Lys His Leu Lys Leu Lys Val Asp Glu	
165 170 175	
ggg gct gat ttt atc gtt act caa atg ttt tat gat gta gac aat ttt	576
Gly Ala Asp Phe Ile Val Thr Gln Met Phe Tyr Asp Val Asp Asn Phe	
180 185 190	
atc gca tgg gtc gat aaa gtg cgt gca gca gga ata aat atc cct ata	624
Ile Ala Trp Val Asp Lys Val Arg Ala Ala Gly Ile Asn Ile Pro Ile	
195 200 205	
ttt ccg ggc att atg cct att cag gca tgg gat tcc ttt att cgg aga	672
Phe Pro Gly Ile Met Pro Ile Gln Ala Trp Asp Ser Phe Ile Arg Arg	
210 215 220	
gcg aaa tgg agc ggt gtt aaa att ccc cag cat ttt atg gat act cta	720
Ala Lys Trp Ser Gly Val Lys Ile Pro Gln His Phe Met Asp Thr Leu	
225 230 235 240	

gtc cca gtt aaa gac gat gat gaa gga gtc cgt gag cgt ggt gtt gag	768
Val Pro Val Lys Asp Asp Asp Glu Gly Val Arg Glu Arg Gly Val Glu	
245 250 255	
ctc ata gtc gaa atg tgc cgt aag ctt ata gct agt ggc att acg aga	816
Leu Ile Val Glu Met Cys Arg Lys Leu Ile Ala Ser Gly Ile Thr Arg	
260 265 270	
ctt cat ttt tac act atg aat tta gaa aag gcc gtt aaa atg att att	864
Leu His Phe Tyr Thr Met Asn Leu Glu Lys Ala Val Lys Met Ile Ile	
275 280 285	
gaa cga tta ggt tta tta gat gaa aac ttg gct cct ata gtg gat act	912
Glu Arg Leu Gly Leu Leu Asp Glu Asn Leu Ala Pro Ile Val Asp Thr	
290 295 300	
aat aac gtc gag tta acc aat gct tcc agt caa gat cgt cgg ata aat	960
Asn Asn Val Glu Leu Thr Asn Ala Ser Ser Gln Asp Arg Arg Ile Asn	
305 310 315 320	
gaa ggt gta cgg ccc att ttc tgg cgc act cgt aat gaa agt tat gtc	1008
Glu Gly Val Arg Pro Ile Phe Trp Arg Thr Arg Asn Glu Ser Tyr Val	
325 330 335	
tcg cgt act gat cag tgg gac gaa tta ccg cat ggt cgt tgg ggt gac	1056
Ser Arg Thr Asp Gln Trp Asp Glu Leu Pro His Gly Arg Trp Gly Asp	
340 345 350	
tct cgt agc cct gct ttt ggc gaa ttt gat gct att aga tat ggt ctt	1104
Ser Arg Ser Pro Ala Phe Gly Glu Phe Asp Ala Ile Arg Tyr Gly Leu	
355 360 365	
cgt atg tct ccc aag gag atc aca aca tcg tgg ggg tct cct aaa tct	1152
Arg Met Ser Pro Lys Glu Ile Thr Thr Ser Trp Gly Ser Pro Lys Ser	
370 375 380	
tac tcg gaa atc ggc gat ttg ttt gcc agg tac tgt gaa aaa aag att	1200
Tyr Ser Glu Ile Gly Asp Leu Phe Ala Arg Tyr Cys Glu Lys Lys Ile	
385 390 395 400	
agc tcc ctc cct tgg agt gat ctt ccc ata tcc gat gaa gcc gac ttg	1248
Ser Ser Leu Pro Trp Ser Asp Leu Pro Ile Ser Asp Glu Ala Asp Leu	
405 410 415	
att cgg gat caa ctt cta agt atg aat aga aac gct ttc ctt act ata	1296
Ile Arg Asp Gln Leu Leu Ser Met Asn Arg Asn Ala Phe Leu Thr Ile	
420 425 430	
aat tct caa cct gct ctt aac ggc gaa aag agt tca cat cct gtt ttt	1344
Asn Ser Gln Pro Ala Leu Asn Gly Glu Lys Ser Ser His Pro Val Phe	
435 440 445	
gga tgg gga cca cct aat ggt tat gtt ttc caa aaa cca tac gtt gag	1392
Gly Trp Gly Pro Pro Asn Gly Tyr Val Phe Gln Lys Pro Tyr Val Glu	
450 455 460	
ttt ttc gtt cac ccc tca ctc ttg aat gaa ctc aaa gaa acc gtt aaa	1440
Phe Phe Val His Pro Ser Leu Leu Asn Glu Leu Lys Glu Thr Val Lys	
465 470 475 480	

aag ctt aat tca gtt tcc tac ttt gtt aca aac aag aat gga gac ttg 1488
 Lys Leu Asn Ser Val Ser Tyr Phe Val Thr Asn Lys Asn Gly Asp Leu
 485 490 495

gat acc aac tca caa tat gag att cca aat gcg gtt aca tgg ggt gtt 1536
 Asp Thr Asn Ser Gln Tyr Glu Ile Pro Asn Ala Val Thr Trp Gly Val
 500 505 510

ttc cct aat cgt gag att atc caa cct act att gtc gag tca acc tct 1584
 Phe Pro Asn Arg Glu Ile Ile Gln Pro Thr Ile Val Glu Ser Thr Ser
 515 520 525

ttt ctt gct tgg aaa gat gaa gcc tat tca ttg ggc atg gaa tgg gct 1632
 Phe Leu Ala Trp Lys Asp Glu Ala Tyr Ser Leu Gly Met Glu Trp Ala
 530 535 540

aat gca tat agc cct gat tca att tct cgt aaa ctt ttg gtt tct atg 1680
 Asn Ala Tyr Ser Pro Asp Ser Ile Ser Arg Lys Leu Leu Val Ser Met
 545 550 555 560

atg aag gaa tgg ttc ctt tgt gtc ata gtt gat aac gat ttt caa aat 1728
 Met Lys Glu Trp Phe Leu Cys Val Ile Val Asp Asn Asp Phe Gln Asn
 565 570 575

ggg caa tct ttg ttt gat gtt ttt aac aaa atg aga tct tta aaa gac 1776
 Gly Gln Ser Leu Phe Asp Val Phe Asn Lys Met Arg Ser Leu Lys Asp
 580 585 590

atc cat cct gag cta tat tat gca aat gca tca taa 1812
 Ile His Pro Glu Leu Tyr Tyr Ala Asn Ala Ser
 595 600

<210> 22

<211> 603

<212> PRT

<213> Schizosaccharomyces pombe

<400> 22

Met Lys Ile Ser Asp Lys Leu Leu His Pro Asp Trp Lys Glu Lys Val
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Thr Tyr Ser Tyr Glu Phe Phe Pro Pro Lys Thr Ser Thr Gly Val Gln
 20 25 30

Asn Leu Tyr Asn Arg Ile Asp Arg Met Lys Thr Trp Gly Arg Pro Met
 35 40 45

Phe Val Asp Val Thr Trp Gly Ala Gly Gly Thr Ser Ser Glu Leu Thr
 50 55 60

Pro Gly Ile Val Asn Val Ile Gln Thr Asp Phe Glu Val Asp Thr Cys
 65 70 75 80

Met His Leu Thr Cys Thr Asn Met Ser Thr Glu Met Ile Asp Ala Ala
 85 90 95

Leu Lys Arg Ala His Glu Thr Gly Cys Arg Asn Ile Leu Ala Leu Arg
 100 105 110

Gly Asp Pro Val Lys Asp Thr Asp Trp Thr Glu Gly Glu Ser Gly Phe
 115 120 125
 Arg Tyr Ala Ser Asp Leu Val Arg Tyr Ile Arg Thr His Tyr Asn Asp
 130 135 140
 Glu Phe Cys Ile Gly Val Ala Gly Tyr Pro Glu Gly Tyr Ser Pro Asp
 145 150 155 160
 Asp Asp Ile Asp Glu Ser Ile Lys His Leu Lys Leu Lys Val Asp Glu
 165 170 175
 Gly Ala Asp Phe Ile Val Thr Gln Met Phe Tyr Asp Val Asp Asn Phe
 180 185 190
 Ile Ala Trp Val Asp Lys Val Arg Ala Ala Gly Ile Asn Ile Pro Ile
 195 200 205
 Phe Pro Gly Ile Met Pro Ile Gln Ala Trp Asp Ser Phe Ile Arg Arg
 210 215 220
 Ala Lys Trp Ser Gly Val Lys Ile Pro Gln His Phe Met Asp Thr Leu
 225 230 235 240
 Val Pro Val Lys Asp Asp Asp Glu Gly Val Arg Glu Arg Gly Val Glu
 245 250 255
 Leu Ile Val Glu Met Cys Arg Lys Leu Ile Ala Ser Gly Ile Thr Arg
 260 265 270
 Leu His Phe Tyr Thr Met Asn Leu Glu Lys Ala Val Lys Met Ile Ile
 275 280 285
 Glu Arg Leu Gly Leu Leu Asp Glu Asn Leu Ala Pro Ile Val Asp Thr
 290 295 300
 Asn Asn Val Glu Leu Thr Asn Ala Ser Ser Gln Asp Arg Arg Ile Asn
 305 310 315 320
 Glu Gly Val Arg Pro Ile Phe Trp Arg Thr Arg Asn Glu Ser Tyr Val
 325 330 335
 Ser Arg Thr Asp Gln Trp Asp Glu Leu Pro His Gly Arg Trp Gly Asp
 340 345 350
 Ser Arg Ser Pro Ala Phe Gly Glu Phe Asp Ala Ile Arg Tyr Gly Leu
 355 360 365
 Arg Met Ser Pro Lys Glu Ile Thr Thr Ser Trp Gly Ser Pro Lys Ser
 370 375 380
 Tyr Ser Glu Ile Gly Asp Leu Phe Ala Arg Tyr Cys Glu Lys Lys Ile
 385 390 395 400
 Ser Ser Leu Pro Trp Ser Asp Leu Pro Ile Ser Asp Glu Ala Asp Leu
 405 410 415
 Ile Arg Asp Gln Leu Leu Ser Met Asn Arg Asn Ala Phe Leu Thr Ile
 420 425 430

Asn Ser Gln Pro Ala Leu Asn Gly Glu Lys Ser Ser His Pro Val Phe
435 440 445

Gly Trp Gly Pro Pro Asn Gly Tyr Val Phe Gln Lys Pro Tyr Val Glu
450 455 460

Phe Phe Val His Pro Ser Leu Leu Asn Glu Leu Lys Glu Thr Val Lys
465 470 475 480

Lys Leu Asn Ser Val Ser Tyr Phe Val Thr Asn Lys Asn Gly Asp Leu
485 490 495

Asp Thr Asn Ser Gln Tyr Glu Ile Pro Asn Ala Val Thr Trp Gly Val
500 505 510

Phe Pro Asn Arg Glu Ile Ile Gln Pro Thr Ile Val Glu Ser Thr Ser
515 520 525

Phe Leu Ala Trp Lys Asp Glu Ala Tyr Ser Leu Gly Met Glu Trp Ala
530 535 540

Asn Ala Tyr Ser Pro Asp Ser Ile Ser Arg Lys Leu Leu Val Ser Met
545 550 555 560

Met Lys Glu Trp Phe Leu Cys Val Ile Val Asp Asn Asp Phe Gln Asn
565 570 575

Gly Gln Ser Leu Phe Asp Val Phe Asn Lys Met Arg Ser Leu Lys Asp
580 585 590

Ile His Pro Glu Leu Tyr Tyr Ala Asn Ala Ser
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<210> 23

<211> 1800

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1797)

<223> RSC08323

<400> 23

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ccc act tac tca ttc gag tac ttc gtc ccg aag act aca caa ggt gta 96
Pro Thr Tyr Ser Phe Glu Tyr Phe Val Pro Lys Thr Thr Gln Gly Val
20 25 30

cag aac ctg tat gac cgg atg gac cgg atg tac gag gct tct ttg ccc 144
Gln Asn Leu Tyr Asp Arg Met Asp Arg Met Tyr Glu Ala Ser Leu Pro
35 40 45

caa ttt att gac atc acc tgg aat gca ggc ggt gga cgg ttg tca cat 192

Gln	Phe	Ile	Asp	Ile	Thr	Trp	Asn	Ala	Gly	Gly	Gly	Arg	Leu	Ser	His		
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ctg	tcc	acg	gac	ttg	gtt	gcg	aca	gcg	cag	tct	gtg	ctt	ggt	ttg	gaa	240	
Leu	Ser	Thr	Asp	Leu	Val	Ala	Thr	Ala	Gln	Ser	Val	Leu	Gly	Leu	Glu		
65					70				75						80		
acg	tgc	atg	cac	ctt	acc	tgc	acc	aat	atg	ccc	att	tcg	atg	att	gac	288	
Thr	Cys	Met	His	Leu	Thr	Cys	Thr	Asn	Met	Pro	Ile	Ser	Met	Ile	Asp		
				85				90						95			
gac	gct	tta	gaa	aac	gct	tat	cac	tcc	ggt	tgc	cag	aac	atc	cta	gcg	336	
Asp	Ala	Leu	Glu	Asn	Ala	Tyr	His	Ser	Gly	Cys	Gln	Asn	Ile	Leu	Ala		
			100					105					110				
ctg	aga	gga	gat	cct	cct	agg	gac	gca	gaa	aac	tgg	act	ccc	gtt	gaa	384	
Leu	Arg	Gly	Asp	Pro	Pro	Arg	Asp	Ala	Glu	Asn	Trp	Thr	Pro	Val	Glu		
		115					120					125					
ggt	ggc	ttc	cag	tat	gcc	aag	gac	ttg	att	aag	tat	atc	aag	tcc	aag	432	
Gly	Gly	Phe	Gln	Tyr	Ala	Lys	Asp	Leu	Ile	Lys	Tyr	Ile	Lys	Ser	Lys		
	130					135					140						
tac	ggt	gac	cat	ttc	gct	atc	ggc	gtt	gcc	ggc	tac	ccg	gag	tgc	cat	480	
Tyr	Gly	Asp	His	Phe	Ala	Ile	Gly	Val	Ala	Gly	Tyr	Pro	Glu	Cys	His		
145					150					155					160		
ccg	gag	ttg	cct	aac	aaa	gac	gtg	aag	ctt	gat	ctc	gag	tat	ttg	agc	528	
Pro	Glu	Leu	Pro	Asn	Lys	Asp	Val	Lys	Leu	Asp	Leu	Glu	Tyr	Leu	Ser		
				165					170					175			
aga	aga	tcg	acc	ggc	ggc	gac	ttc	atc	atc	act	cag	atg	ttt	tac	gat	576	
Arg	Arg	Ser	Thr	Gly	Gly	Asp	Phe	Ile	Ile	Thr	Gln	Met	Phe	Tyr	Asp		
			180					185					190				
gtt	gat	aat	tta	ctc	aac	tgg	tgt	tcc	caa	gtt	aga	gct	gcg	ggc	atg	624	
Val	Asp	Asn	Leu	Leu	Asn	Trp	Cys	Ser	Gln	Val	Arg	Ala	Ala	Gly	Met		
		195				200						205					
gac	gtg	ccc	att	att	ccc	ggg	atc	atg	ccg	atc	act	acc	tac	gcg	gcc	672	
Asp	Val	Pro	Ile	Ile	Pro	Gly	Ile	Met	Pro	Ile	Thr	Thr	Tyr	Ala	Ala		
	210					215					220						
ttc	ttg	aga	agg	atc	caa	tgg	ggc	caa	atc	tcc	atc	cct	caa	cat	ttc	720	
Phe	Leu	Arg	Arg	Ile	Gln	Trp	Gly	Gln	Ile	Ser	Ile	Pro	Gln	His	Phe		
225					230					235					240		
tcg	tcc	cga	ttg	gat	cct	atc	aag	gac	gat	gac	gag	ttg	gtc	cgt	gat	768	
Ser	Ser	Arg	Leu	Asp	Pro	Ile	Lys	Asp	Asp	Asp	Glu	Leu	Val	Arg	Asp		
				245				250						255			
atc	gga	act	aac	ttg	atc	gtg	gaa	atg	tgt	caa	aaa	ttg	ctc	gac	agt	816	
Ile	Gly	Thr	Asn	Leu	Ile	Val	Glu	Met	Cys	Gln	Lys	Leu	Leu	Asp	Ser		
			260					265					270				
ggt	tac	gtt	tct	cac	ttg	cac	atc	tac	acc	atg	aac	ttg	gaa	aaa	gcg	864	
Gly	Tyr	Val	Ser	His	Leu	His	Ile	Tyr	Thr	Met	Asn	Leu	Glu	Lys	Ala		
		275					280					285					
cct	ctc	atg	att	ctg	gaa	aga	ttg	aac	att	cta	cct	acg	gaa	tca	gag	912	

Pro	Leu	Met	Ile	Leu	Glu	Arg	Leu	Asn	Ile	Leu	Pro	Thr	Glu	Ser	Glu	
290						295				300						
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Phe	Asn	Ala	His	Pro	Leu	Ala	Val	Leu	Pro	Trp	Arg	Lys	Ser	Leu	Asn	
305					310				315						320	
cca	aag	cgt	aaa	aac	gag	gaa	gtc	aga	cct	atc	ttc	tgg	aag	aga	aga	1008
Pro	Lys	Arg	Lys	Asn	Glu	Glu	Val	Arg	Pro	Ile	Phe	Trp	Lys	Arg	Arg	
				325					330					335		
cct	tac	tcc	tat	gtc	gca	aga	acc	tct	caa	tgg	gcc	gtg	gac	gaa	ttc	1056
Pro	Tyr	Ser	Tyr	Val	Ala	Arg	Thr	Ser	Gln	Trp	Ala	Val	Asp	Glu	Phe	
			340					345					350			
ccc	aac	ggt	aga	ttc	ggt	gat	tcg	tct	tct	cct	gcg	ttc	ggt	gac	ttg	1104
Pro	Asn	Gly	Arg	Phe	Gly	Asp	Ser	Ser	Ser	Pro	Ala	Phe	Gly	Asp	Leu	
		355					360					365				
gat	ctg	tgt	ggt	tca	gac	ttg	atc	agg	caa	tca	gcg	aac	aaa	tgt	ctc	1152
Asp	Leu	Cys	Gly	Ser	Asp	Leu	Ile	Arg	Gln	Ser	Ala	Asn	Lys	Cys	Leu	
	370					375					380					
gaa	tta	tgg	tcc	acc	cct	act	tcc	atc	aac	gac	gtc	gcc	ttc	ttg	gtc	1200
Glu	Leu	Trp	Ser	Thr	Pro	Thr	Ser	Ile	Asn	Asp	Val	Ala	Phe	Leu	Val	
385					390					395					400	
atc	aac	tac	ttg	aat	gga	aac	ttg	aag	tgt	tta	cct	tgg	agt	gat	atc	1248
Ile	Asn	Tyr	Leu	Asn	Gly	Asn	Leu	Lys	Cys	Leu	Pro	Trp	Ser	Asp	Ile	
				405				410						415		
ccc	atc	aat	gat	gaa	ata	aat	cca	atc	aaa	gca	cac	ttg	att	gag	ctg	1296
Pro	Ile	Asn	Asp	Glu	Ile	Asn	Pro	Ile	Lys	Ala	His	Leu	Ile	Glu	Leu	
			420					425					430			
aac	cag	cat	tct	atc	atc	act	ata	aac	tct	caa	cct	caa	gtc	aac	ggc	1344
Asn	Gln	His	Ser	Ile	Ile	Thr	Ile	Asn	Ser	Gln	Pro	Gln	Val	Asn	Gly	
		435					440					445				
att	agg	tcc	aat	gac	aaa	att	cat	ggt	tgg	gga	ccc	aag	gat	ggt	tac	1392
Ile	Arg	Ser	Asn	Asp	Lys	Ile	His	Gly	Trp	Gly	Pro	Lys	Asp	Gly	Tyr	
	450					455				460						
gtt	tac	cag	aag	caa	tat	ttg	gaa	ttt	atg	ttg	ccc	aag	act	aag	ttg	1440
Val	Tyr	Gln	Lys	Gln	Tyr	Leu	Glu	Phe	Met	Leu	Pro	Lys	Thr	Lys	Leu	
465					470				475						480	
ccc	aag	ttg	att	gac	acc	ttg	aaa	aac	aat	gag	ttc	ttg	acc	tac	ttc	1488
Pro	Lys	Leu	Ile	Asp	Thr	Leu	Lys	Asn	Asn	Glu	Phe	Leu	Thr	Tyr	Phe	
				485					490					495		
gcc	atc	gac	tct	caa	ggt	gac	ctg	cta	agt	aat	cat	cca	gac	aac	tcc	1536
Ala	Ile	Asp	Ser	Gln	Gly	Asp	Leu	Leu	Ser	Asn	His	Pro	Asp	Asn	Ser	
			500					505					510			
aag	tcc	aac	gct	gtg	act	tgg	ggt	att	ttc	ccc	ggc	aga	gaa	att	ctt	1584
Lys	Ser	Asn	Ala	Val	Thr	Trp	Gly	Ile	Phe	Pro	Gly	Arg	Glu	Ile	Leu	
		515					520					525				
caa	cct	acc	att	gtc	gag	aaa	att	tcg	ttc	tta	gcg	tgg	aag	gag	gag	1632

Gln Pro Thr Ile Val Glu Lys Ile Ser Phe Leu Ala Trp Lys Glu Glu
 530 535 540

ttc tat cat atc ttg aat gaa tgg aaa cta aac atg aat aaa tac gat 1680
 Phe Tyr His Ile Leu Asn Glu Trp Lys Leu Asn Met Asn Lys Tyr Asp
 545 550 555 560

aaa ccg cat agt gcc caa ttc att cag tcc ttg att gac gat tac tgc 1728
 Lys Pro His Ser Ala Gln Phe Ile Gln Ser Leu Ile Asp Asp Tyr Cys
 565 570 575

ttg gtc aat att gtt gac aat gac tac att tct cca gat gat caa atc 1776
 Leu Val Asn Ile Val Asp Asn Asp Tyr Ile Ser Pro Asp Asp Gln Ile
 580 585 590

cat tcc atc cta cta agc cta taa 1800
 His Ser Ile Leu Leu Ser Leu
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<210> 24
 <211> 599
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 24
 Met Lys Ile Thr Glu Lys Leu Glu Gln His Arg Gln Thr Ser Gly Lys
 1 5 10 15

Pro Thr Tyr Ser Phe Glu Tyr Phe Val Pro Lys Thr Thr Gln Gly Val
 20 25 30

Gln Asn Leu Tyr Asp Arg Met Asp Arg Met Tyr Glu Ala Ser Leu Pro
 35 40 45

Gln Phe Ile Asp Ile Thr Trp Asn Ala Gly Gly Gly Arg Leu Ser His
 50 55 60

Leu Ser Thr Asp Leu Val Ala Thr Ala Gln Ser Val Leu Gly Leu Glu
 65 70 75 80

Thr Cys Met His Leu Thr Cys Thr Asn Met Pro Ile Ser Met Ile Asp
 85 90 95

Asp Ala Leu Glu Asn Ala Tyr His Ser Gly Cys Gln Asn Ile Leu Ala
 100 105 110

Leu Arg Gly Asp Pro Pro Arg Asp Ala Glu Asn Trp Thr Pro Val Glu
 115 120 125

Gly Gly Phe Gln Tyr Ala Lys Asp Leu Ile Lys Tyr Ile Lys Ser Lys
 130 135 140

Tyr Gly Asp His Phe Ala Ile Gly Val Ala Gly Tyr Pro Glu Cys His
 145 150 155 160

Pro Glu Leu Pro Asn Lys Asp Val Lys Leu Asp Leu Glu Tyr Leu Ser
 165 170 175

Arg Arg Ser Thr Gly Gly Asp Phe Ile Ile Thr Gln Met Phe Tyr Asp

180					185					190						
Val	Asp	Asn	Leu	Leu	Asn	Trp	Cys	Ser	Gln	Val	Arg	Ala	Ala	Gly	Met	
195					200					205						
Asp	Val	Pro	Ile	Ile	Pro	Gly	Ile	Met	Pro	Ile	Thr	Thr	Tyr	Ala	Ala	
210					215					220						
Phe	Leu	Arg	Arg	Ile	Gln	Trp	Gly	Gln	Ile	Ser	Ile	Pro	Gln	His	Phe	
225					230					235					240	
Ser	Ser	Arg	Leu	Asp	Pro	Ile	Lys	Asp	Asp	Asp	Glu	Leu	Val	Arg	Asp	
245					250					255						
Ile	Gly	Thr	Asn	Leu	Ile	Val	Glu	Met	Cys	Gln	Lys	Leu	Leu	Asp	Ser	
260					265					270						
Gly	Tyr	Val	Ser	His	Leu	His	Ile	Tyr	Thr	Met	Asn	Leu	Glu	Lys	Ala	
275					280					285						
Pro	Leu	Met	Ile	Leu	Glu	Arg	Leu	Asn	Ile	Leu	Pro	Thr	Glu	Ser	Glu	
290					295					300						
Phe	Asn	Ala	His	Pro	Leu	Ala	Val	Leu	Pro	Trp	Arg	Lys	Ser	Leu	Asn	
305					310					315					320	
Pro	Lys	Arg	Lys	Asn	Glu	Glu	Val	Arg	Pro	Ile	Phe	Trp	Lys	Arg	Arg	
325					330					335						
Pro	Tyr	Ser	Tyr	Val	Ala	Arg	Thr	Ser	Gln	Trp	Ala	Val	Asp	Glu	Phe	
340					345					350						
Pro	Asn	Gly	Arg	Phe	Gly	Asp	Ser	Ser	Ser	Pro	Ala	Phe	Gly	Asp	Leu	
355					360					365						
Asp	Leu	Cys	Gly	Ser	Asp	Leu	Ile	Arg	Gln	Ser	Ala	Asn	Lys	Cys	Leu	
370					375					380						
Glu	Leu	Trp	Ser	Thr	Pro	Thr	Ser	Ile	Asn	Asp	Val	Ala	Phe	Leu	Val	
385					390					395					400	
Ile	Asn	Tyr	Leu	Asn	Gly	Asn	Leu	Lys	Cys	Leu	Pro	Trp	Ser	Asp	Ile	
405					410					415						
Pro	Ile	Asn	Asp	Glu	Ile	Asn	Pro	Ile	Lys	Ala	His	Leu	Ile	Glu	Leu	
420					425					430						
Asn	Gln	His	Ser	Ile	Ile	Thr	Ile	Asn	Ser	Gln	Pro	Gln	Val	Asn	Gly	
435					440					445						
Ile	Arg	Ser	Asn	Asp	Lys	Ile	His	Gly	Trp	Gly	Pro	Lys	Asp	Gly	Tyr	
450					455					460						
Val	Tyr	Gln	Lys	Gln	Tyr	Leu	Glu	Phe	Met	Leu	Pro	Lys	Thr	Lys	Leu	
465					470					475					480	
Pro	Lys	Leu	Ile	Asp	Thr	Leu	Lys	Asn	Asn	Glu	Phe	Leu	Thr	Tyr	Phe	
485					490					495						
Ala	Ile	Asp	Ser	Gln	Gly	Asp	Leu	Leu	Ser	Asn	His	Pro	Asp	Asn	Ser	

500	505	510
Lys Ser Asn Ala Val Thr Trp Gly Ile Phe Pro Gly Arg Glu Ile Leu 515	520	525
Gln Pro Thr Ile Val Glu Lys Ile Ser Phe Leu Ala Trp Lys Glu Glu 530	535	540
Phe Tyr His Ile Leu Asn Glu Trp Lys Leu Asn Met Asn Lys Tyr Asp 545	550	555
Lys Pro His Ser Ala Gln Phe Ile Gln Ser Leu Ile Asp Asp Tyr Cys 565	570	575
Leu Val Asn Ile Val Asp Asn Asp Tyr Ile Ser Pro Asp Asp Gln Ile 580	585	590
His Ser Ile Leu Leu Ser Leu 595		

<210> 25
 <211> 897
 <212> DNA
 <213> Erwinia carotovora

<220>
 <221> CDS
 <222> (1) .. (894)
 <223> RE000089

<400> 25
 atg agc ttt ttt cac gca aac cag cgg gaa gcg ctg aat caa agt ctg 48
 Met Ser Phe Phe His Ala Asn Gln Arg Glu Ala Leu Asn Gln Ser Leu
 1 5 10 15

gcg gaa ttg cag gga cga att aat gtg tca ttt gaa ttt ttc ccg cca 96
 Ala Glu Leu Gln Gly Arg Ile Asn Val Ser Phe Glu Phe Phe Pro Pro
 20 25 30

cgt acc agc gat atg gaa gaa acc ctg tgg agc tct atc gat cga ctg 144
 Arg Thr Ser Asp Met Glu Glu Thr Leu Trp Ser Ser Ile Asp Arg Leu
 35 40 45

agc agc ctg aag ccc aag ttt gtt tcc gtg act tac ggg gcg aat tct 192
 Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser
 50 55 60

ggc gag cgt gac cgt act cac agc att atc aaa acg att aaa gag cgt 240
 Gly Glu Arg Asp Arg Thr His Ser Ile Ile Lys Thr Ile Lys Glu Arg
 65 70 75 80

acc ggt ctg gaa gcg gca cct cac ctg acc tgc atc gat gct tca cgc 288
 Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Ser Arg
 85 90 95

gaa cag ctg cgt gaa atc gct cag gat tac tgg gag agt ggt atc cgc 336
 Glu Gln Leu Arg Glu Ile Ala Gln Asp Tyr Trp Glu Ser Gly Ile Arg
 100 105 110

cat att gtc gcg ctg cgc ggc gac ttg cct caa gaa ggc ggc aaa ccg 384
 His Ile Val Ala Leu Arg Gly Asp Leu Pro Gln Glu Gly Gly Lys Pro
 115 120 125

gac atg tac gcg gcg gat ctg gtt tcc ctg ctg aaa gag gtc ggt gat 432
 Asp Met Tyr Ala Ala Asp Leu Val Ser Leu Leu Lys Glu Val Gly Asp
 130 135 140

ttc gat att tcc gtt gcc gcc tat cct gaa gta cac cct gaa gcg aaa 480
 Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys
 145 150 155 160

agc gcg cag gct gac ctg att aac ctg aaa cac aag att gat gcc ggc 528
 Ser Ala Gln Ala Asp Leu Ile Asn Leu Lys His Lys Ile Asp Ala Gly
 165 170 175

gcg aat cgc gct atc aca cag ttc ttt ttc gac gta gaa agc tat ttg 576
 Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu
 180 185 190

cgg ttc cgt gac cgc tgc gtg gca acg ggc atc gat gta gaa att gtg 624
 Arg Phe Arg Asp Arg Cys Val Ala Thr Gly Ile Asp Val Glu Ile Val
 195 200 205

ccg ggc att ctg cca gta tgc aac ttc aaa cag ttg cag aaa ttt gcc 672
 Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Leu Gln Lys Phe Ala
 210 215 220

acg atg acc aac gtc cgt gtg ccg aac tgg atg acg acc atg ttt gac 720
 Thr Met Thr Asn Val Arg Val Pro Asn Trp Met Thr Thr Met Phe Asp
 225 230 235 240

ggc ctg gat aac gat cca gaa acc cgc aaa atg gtg ggg gcg tct atc 768
 Gly Leu Asp Asn Asp Pro Glu Thr Arg Lys Met Val Gly Ala Ser Ile
 245 250 255

gcc atg gat atg gtg aaa att ctc agc cgc gaa ggc gta aaa gat ttc 816
 Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe
 260 265 270

cat ttc tat acg ctg aac cgc gcg gag ctg agc tat gcg att tgc cat 864
 His Phe Tyr Thr Leu Asn Arg Ala Glu Leu Ser Tyr Ala Ile Cys His
 275 280 285

acg ctg ggc gtc cgc cct gat gta gca cgc tga 897
 Thr Leu Gly Val Arg Pro Asp Val Ala Arg
 290 295

<210> 26

<211> 298

<212> PRT

<213> *Erwinia carotovora*

<400> 26

Met Ser Phe Phe His Ala Asn Gln Arg Glu Ala Leu Asn Gln Ser Leu
 1 5 10 15

Ala Glu Leu Gln Gly Arg Ile Asn Val Ser Phe Glu Phe Phe Pro Pro
 20 25 30

Arg	Thr	Ser	Asp	Met	Glu	Glu	Thr	Leu	Trp	Ser	Ser	Ile	Asp	Arg	Leu
		35					40					45			
Ser	Ser	Leu	Lys	Pro	Lys	Phe	Val	Ser	Val	Thr	Tyr	Gly	Ala	Asn	Ser
	50					55					60				
Gly	Glu	Arg	Asp	Arg	Thr	His	Ser	Ile	Ile	Lys	Thr	Ile	Lys	Glu	Arg
65					70					75					80
Thr	Gly	Leu	Glu	Ala	Ala	Pro	His	Leu	Thr	Cys	Ile	Asp	Ala	Ser	Arg
				85					90					95	
Glu	Gln	Leu	Arg	Glu	Ile	Ala	Gln	Asp	Tyr	Trp	Glu	Ser	Gly	Ile	Arg
			100					105					110		
His	Ile	Val	Ala	Leu	Arg	Gly	Asp	Leu	Pro	Gln	Glu	Gly	Gly	Lys	Pro
		115					120					125			
Asp	Met	Tyr	Ala	Ala	Asp	Leu	Val	Ser	Leu	Leu	Lys	Glu	Val	Gly	Asp
		130				135					140				
Phe	Asp	Ile	Ser	Val	Ala	Ala	Tyr	Pro	Glu	Val	His	Pro	Glu	Ala	Lys
145					150					155					160
Ser	Ala	Gln	Ala	Asp	Leu	Ile	Asn	Leu	Lys	His	Lys	Ile	Asp	Ala	Gly
				165					170					175	
Ala	Asn	Arg	Ala	Ile	Thr	Gln	Phe	Phe	Phe	Asp	Val	Glu	Ser	Tyr	Leu
			180					185					190		
Arg	Phe	Arg	Asp	Arg	Cys	Val	Ala	Thr	Gly	Ile	Asp	Val	Glu	Ile	Val
		195					200					205			
Pro	Gly	Ile	Leu	Pro	Val	Ser	Asn	Phe	Lys	Gln	Leu	Gln	Lys	Phe	Ala
	210					215					220				
Thr	Met	Thr	Asn	Val	Arg	Val	Pro	Asn	Trp	Met	Thr	Thr	Met	Phe	Asp
225				230						235					240
Gly	Leu	Asp	Asn	Asp	Pro	Glu	Thr	Arg	Lys	Met	Val	Gly	Ala	Ser	Ile
				245					250					255	
Ala	Met	Asp	Met	Val	Lys	Ile	Leu	Ser	Arg	Glu	Gly	Val	Lys	Asp	Phe
			260					265					270		
His	Phe	Tyr	Thr	Leu	Asn	Arg	Ala	Glu	Leu	Ser	Tyr	Ala	Ile	Cys	His
		275					280					285			
Thr	Leu	Gly	Val	Arg	Pro	Asp	Val	Ala	Arg						
	290					295									

<210> 27

<211> 888

<212> DNA

<213> Klebsiella pneumoniae

<220>

<221> CDS

<222> (1)..(885)

<223> RKP07488

<400> 27

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Met Ser Phe Phe His Ala Asn Gln Arg Glu Ala Leu Asn Gln Ser Leu	
1 5 10 15	
gcg gaa gtc cag ggc cag att aat gtg tct ttt gaa ttc ttt ccg ccg	96
Ala Glu Val Gln Gly Gln Ile Asn Val Ser Phe Glu Phe Phe Pro Pro	
20 25 30	
cgc acc agt gaa atg gag caa acc ctg tgg aaa tcc atc gat cgc ctg	144
Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Lys Ser Ile Asp Arg Leu	
35 40 45	
agc agt ctg aaa ccg aag ttt gtt tcg gta acc tat ggc gcg aac tct	192
Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser	
50 55 60	
ggc gag cgc gat cgc acc cac agc atc atc aaa ggc att aaa gag cga	240
Gly Glu Arg Asp Arg Thr His Ser Ile Ile Lys Gly Ile Lys Glu Arg	
65 70 75 80	
acc ggt ctg gaa gca gcg ccg cac ctg acc tgt atc gat gcc agc cgc	288
Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Ser Arg	
85 90 95	
gat gag ttg cgc act atc gct cag gat tac tgg aac aac ggt atc cgc	336
Asp Glu Leu Arg Thr Ile Ala Gln Asp Tyr Trp Asn Asn Gly Ile Arg	
100 105 110	
cat atc gtc gcc ctg cgc ggc gac ctg ccg ccg ggc agc ggt aaa ccg	384
His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro	
115 120 125	
gat atg tac gcc gcc gat ctg gtg acg ttg ctg aaa gag gta ggc gat	432
Asp Met Tyr Ala Ala Asp Leu Val Thr Leu Leu Lys Glu Val Gly Asp	
130 135 140	
ttt gat atc tct gtc gcc gcg tat ccg gaa gtg cat ccg gag gcg aaa	480
Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys	
145 150 155 160	
agc gcg cag gcg gat tta ctg aac ctg aag cgc aaa gta gaa gca ggg	528
Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Glu Ala Gly	
165 170 175	
gcc aac cgc gcg atc acc cag ttc ttc ttc gat gtg gaa agc tac ctg	576
Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu	
180 185 190	
cgt ttt cgc gat cgc tgc gtc tcg gca ggc atc gac gtg gaa atc att	624
Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile	
195 200 205	
ccc ggt atc ctg ccg gtc tcc aac ttt aaa cag gcg aaa aag ttt gcg	672
Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala	
210 215 220	

gat atg acc aac gtc cgt atc ccg gtg tgg atg tca aaa atg ttc gaa 720
 Asp Met Thr Asn Val Arg Ile Pro Val Trp Met Ser Lys Met Phe Glu
 225 230 235 240

ggg ctg gat aac gac gcc gaa acc cgt caa ctg gtg ggg gcg aat atc 768
 Gly Leu Asp Asn Asp Ala Glu Thr Arg Gln Leu Val Gly Ala Asn Ile
 245 250 255

gcc atg gac atg gtg aag atc tta agc cgg gaa ggg gtc aag gat ttc 816
 Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe
 260 265 270

cac ttc tac acc ctg aac cgc gcc gag atg agc tac gcc atc tgc cat 864
 His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His
 275 280 285

acg ctg ggc gta cgc ccg gcc tga 888
 Thr Leu Gly Val Arg Pro Ala
 290 295

<210> 28

<211> 295

<212> PRT

<213> *Klebsiella pneumoniae*

<400> 28

Met Ser Phe Phe His Ala Asn Gln Arg Glu Ala Leu Asn Gln Ser Leu
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Ala Glu Val Gln Gly Gln Ile Asn Val Ser Phe Glu Phe Phe Pro Pro
 20 25 30

Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Lys Ser Ile Asp Arg Leu
 35 40 45

Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser
 50 55 60

Gly Glu Arg Asp Arg Thr His Ser Ile Ile Lys Gly Ile Lys Glu Arg
 65 70 75 80

Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Ser Arg
 85 90 95

Asp Glu Leu Arg Thr Ile Ala Gln Asp Tyr Trp Asn Asn Gly Ile Arg
 100 105 110

His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro
 115 120 125

Asp Met Tyr Ala Ala Asp Leu Val Thr Leu Leu Lys Glu Val Gly Asp
 130 135 140

Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys
 145 150 155 160

Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Glu Ala Gly
 165 170 175

Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu
180 185 190

Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile
195 200 205

Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala
210 215 220

Asp Met Thr Asn Val Arg Ile Pro Val Trp Met Ser Lys Met Phe Glu
225 230 235 240

Gly Leu Asp Asn Asp Ala Glu Thr Arg Gln Leu Val Gly Ala Asn Ile
245 250 255

Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe
260 265 270

His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His
275 280 285

Thr Leu Gly Val Arg Pro Ala
290 295

<210> 29

<211> 891

<212> DNA

<213> Salmonella typhi

<220>

<221> CDS

<222> (1)..(888)

<223> RTY02485

<400> 29

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1 5 10 15

gcg gaa gta cag ggt cag att aac gtt tcg ttt gaa ttt ttc ccg ccg 96
Ala Glu Val Gln Gly Gln Ile Asn Val Ser Phe Glu Phe Phe Pro Pro
20 25 30

cgc acc agt gaa atg gag caa acc ctg tgg aac tcc atc gat cgc ctg 144
Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Asn Ser Ile Asp Arg Leu
35 40 45

agc agc ctg aaa ccg aag ttt gtt tcg gta acg tat ggc gcc aac tcc 192
Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser
50 55 60

ggg gaa cgt gac cgc act cat agt gtt att aaa ggc att aaa gag cgt 240
Gly Glu Arg Asp Arg Thr His Ser Val Ile Lys Gly Ile Lys Glu Arg
65 70 75 80

act ggg ctt gag gcc gcg ccg cac ctt acc tgt att gac gcc acg cgc 288
Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Thr Arg
85 90 95

gat gaa ctg cgc acc atc gcc cgc gac tac tgg aat aac ggt atc cgc	336
Asp Glu Leu Arg Thr Ile Ala Arg Asp Tyr Trp Asn Asn Gly Ile Arg	
100 105 110	
 cac att gtt gct ttg cgc ggc gat ttg ccg ccg ggc agc ggt aag ccg	384
His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro	
115 120 125	
 gag atg tac gcc gcc gat ctg gtt ggt ttg ctc aaa gag gtg gtc gat	432
Glu Met Tyr Ala Ala Asp Leu Val Gly Leu Leu Lys Glu Val Val Asp	
130 135 140	
 ttc gat att tca gta gcg gcc tat ccg gag gta cat ccg gaa gcg aaa	480
Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys	
145 150 155 160	
 agc gcg cag gcc gat ctg ctt aat ctg aag cgt aaa gtg gat gct ggc	528
Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Asp Ala Gly	
165 170 175	
 gct aac cgc gcg ata acc caa ttt ttc ttc gat gtg gaa agc tat ctg	576
Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu	
180 185 190	
 cgt ttt cgc gac cgc tgt gtt tcc gcc ggt atc gac gta gaa att att	624
Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile	
195 200 205	
 ccc ggc att tta ccg gtg tct aac ttt aaa cag gcg aaa aaa ttt gcc	672
Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala	
210 215 220	
 gat atg acc aat gtc cgc att ccg tcc tgg atg tcg ctg atg ttt gag	720
Asp Met Thr Asn Val Arg Ile Pro Ser Trp Met Ser Leu Met Phe Glu	
225 230 235 240	
 ggg ctg gat gat gac gca gaa acc cgc aag ctg gtg ggc gct aac att	768
Gly Leu Asp Asp Asp Ala Glu Thr Arg Lys Leu Val Gly Ala Asn Ile	
245 250 255	
 gcg atg gac atg gtg aaa att tta agc cgc gaa gga gtg aag gat ttc	816
Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe	
260 265 270	
 cac ttc tac acg ttg aat cgt gcg gaa atg agt tat gcc att tgc cac	864
His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His	
275 280 285	
 acg ctg ggc gta aga ccg ggt tta taa	891
Thr Leu Gly Val Arg Pro Gly Leu	
290 295	

<210> 30

<211> 296

<212> PRT

<213> Salmonella typhi

<400> 30

Met Ser Phe Phe His Ala Asn Gln Arg Glu Ala Leu Asn Gln Ser Leu

1	5	10	15
Ala Glu Val Gln Gly Gln Ile Asn Val Ser Phe Glu Phe Phe Pro Pro	20	25	30
Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Asn Ser Ile Asp Arg Leu	35	40	45
Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser	50	55	60
Gly Glu Arg Asp Arg Thr His Ser Val Ile Lys Gly Ile Lys Glu Arg	65	70	75
Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Thr Arg	85	90	95
Asp Glu Leu Arg Thr Ile Ala Arg Asp Tyr Trp Asn Asn Gly Ile Arg	100	105	110
His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro	115	120	125
Glu Met Tyr Ala Ala Asp Leu Val Gly Leu Leu Lys Glu Val Val Asp	130	135	140
Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys	145	150	155
Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Asp Ala Gly	165	170	175
Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu	180	185	190
Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile	195	200	205
Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala	210	215	220
Asp Met Thr Asn Val Arg Ile Pro Ser Trp Met Ser Leu Met Phe Glu	225	230	235
Gly Leu Asp Asp Asp Ala Glu Thr Arg Lys Leu Val Gly Ala Asn Ile	245	250	255
Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe	260	265	270
His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His	275	280	285
Thr Leu Gly Val Arg Pro Gly Leu	290	295	

<210> 31
 <211> 891
 <212> DNA

<213> *Salmonella typhimurium*

<220>

<221> CDS

<222> (1)..(888)

<223> RSY00593

<400> 31

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Met Ser Phe Phe His Ala Asn Gln Arg Glu Ala Leu Asn Gln Ser Leu	
1 5 10 15	
gcg gaa gta cag ggt cag att aac gtt tcg ttt gaa ttt ttc ccg ccg	96
Ala Glu Val Gln Gly Gln Ile Asn Val Ser Phe Glu Phe Phe Pro Pro	
20 25 30	
cgc acc agt gaa atg gag caa acc ctg tgg aac tcc atc gat cgc ctg	144
Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Asn Ser Ile Asp Arg Leu	
35 40 45	
agc agt ctg aaa ccg aag ttt gtt tcg gta acg tat ggc gcc aac tcc	192
Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser	
50 55 60	
ggg gaa cgc gac cgc acc cat agc gtt att aaa ggc atc aaa gag cgt	240
Gly Glu Arg Asp Arg Thr His Ser Val Ile Lys Gly Ile Lys Glu Arg	
65 70 75 80	
act ggg ctt gag gcc gcg ccg cac ctt acc tgt att gac gcc acg cgc	288
Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Thr Arg	
85 90 95	
gat gaa ctg cgc acc atc gcc cgc gac tac tgg aat aac ggt atc cgc	336
Asp Glu Leu Arg Thr Ile Ala Arg Asp Tyr Trp Asn Asn Gly Ile Arg	
100 105 110	
cac att gtc gct ttg cgc ggc gat ttg ccg ccg ggc agc ggt aag ccg	384
His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro	
115 120 125	
gag atg tac gcc gcc gat ctg gtt ggt ttg ctc aaa gag gtg gcc gat	432
Glu Met Tyr Ala Ala Asp Leu Val Gly Leu Leu Lys Glu Val Ala Asp	
130 135 140	
ttc gat att tca gta gcg gcc tat ccg gag gta cat ccg gaa gcg aaa	480
Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys	
145 150 155 160	
agc gcg cag gcc gat ctg ctt aat ctg aag cgt aaa gtg gat gct ggc	528
Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Asp Ala Gly	
165 170 175	
gct aac cgc gcg ata acc caa ttt ttc ttc gat gtg gaa agc tac ctg	576
Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu	
180 185 190	
cgt ttt cgc gac cgc tgt gtt tct gcc ggt atc gac gta gaa att att	624
Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile	
195 200 205	

ccc ggc att tta ccg gtg tct aac ttt aaa cag gca aaa aaa ttt gcc 672
 Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala
 210 215 220

gat atg acc aat gtc cgc att ccg tcc tgg atg tca ctg atg ttt gag 720
 Asp Met Thr Asn Val Arg Ile Pro Ser Trp Met Ser Leu Met Phe Glu
 225 230 235 240

ggg ctg gat aat gac gca gaa acc cgc aag ctg gtg ggc gct aac att 768
 Gly Leu Asp Asn Asp Ala Glu Thr Arg Lys Leu Val Gly Ala Asn Ile
 245 250 255

gcg atg gac atg gtg aaa att tta agc cgt gaa gga gtg aag gat ttc 816
 Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe
 260 265 270

cac ttc tac acg ttg aat cgt gcg gaa atg agt tat gcc att tgc cac 864
 His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His
 275 280 285

acg ctg ggc gta aga ccg ggt tta taa 891
 Thr Leu Gly Val Arg Pro Gly Leu
 290 295

<210> 32

<211> 296

<212> PRT

<213> Salmonella typhimurium

<400> 32

Met Ser Phe Phe His Ala Asn Gln Arg Glu Ala Leu Asn Gln Ser Leu
 1 5 10 15

Ala Glu Val Gln Gly Gln Ile Asn Val Ser Phe Glu Phe Phe Pro Pro
 20 25 30

Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Asn Ser Ile Asp Arg Leu
 35 40 45

Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser
 50 55 60

Gly Glu Arg Asp Arg Thr His Ser Val Ile Lys Gly Ile Lys Glu Arg
 65 70 75 80

Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Thr Arg
 85 90 95

Asp Glu Leu Arg Thr Ile Ala Arg Asp Tyr Trp Asn Asn Gly Ile Arg
 100 105 110

His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro
 115 120 125

Glu Met Tyr Ala Ala Asp Leu Val Gly Leu Leu Lys Glu Val Ala Asp
 130 135 140

Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys
 145 150 155 160

Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Asp Ala Gly
 165 170 175
 Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu
 180 185 190
 Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile
 195 200 205
 Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala
 210 215 220
 Asp Met Thr Asn Val Arg Ile Pro Ser Trp Met Ser Leu Met Phe Glu
 225 230 235 240
 Gly Leu Asp Asn Asp Ala Glu Thr Arg Lys Leu Val Gly Ala Asn Ile
 245 250 255
 Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe
 260 265 270
 His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His
 275 280 285
 Thr Leu Gly Val Arg Pro Gly Leu
 290 295

<210> 33
 <211> 891
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(888)
 <223> REC03839

<400> 33
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 1 5 10 15
 gca gaa gtc cag ggg cag att aac gtt tcg ttc gag ttt ttc ccg ccg 96
 Ala Glu Val Gln Gly Gln Ile Asn Val Ser Phe Glu Phe Phe Pro Pro
 20 25 30
 cgt acc agt gaa atg gag cag acc ctg tgg aac tcc atc gat cgc ctt 144
 Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Asn Ser Ile Asp Arg Leu
 35 40 45
 agc agc ctg aaa ccg aag ttt gta tcg gtg acc tat ggc gcg aac tcc 192
 Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser
 50 55 60
 ggc gag cgc gac cgt acg cac agc att att aaa ggc att aaa gat cgc 240
 Gly Glu Arg Asp Arg Thr His Ser Ile Ile Lys Gly Ile Lys Asp Arg
 65 70 75 80

act ggt ctg gaa gcg gca ccg cat ctt act tgc att gat gcg acg ccc	288
Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Thr Pro	
85 90 95	
gac gag ctg cgc acc att gca cgc gac tac tgg aat aac ggt att cgt	336
Asp Glu Leu Arg Thr Ile Ala Arg Asp Tyr Trp Asn Asn Gly Ile Arg	
100 105 110	
cat atc gtg gcg ctg cgt ggc gat ctg ccg ccg gga agt ggt aag cca	384
His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro	
115 120 125	
gaa atg tat gct tct gac ctg gtg acg ctg tta aaa gaa gtg gca gat	432
Glu Met Tyr Ala Ser Asp Leu Val Thr Leu Leu Lys Glu Val Ala Asp	
130 135 140	
ttc gat atc tcc gtg gcg gcg tat ccg gaa gtt cac ccg gaa gca aaa	480
Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys	
145 150 155 160	
agc gct cag gcg gat ttg ctt aat ctg aaa cgc aaa gtg gat gcc gga	528
Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Asp Ala Gly	
165 170 175	
gcc aac cgc gcg att act cag ttc ttc ttc gat gtc gaa agc tac ctg	576
Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu	
180 185 190	
cgt ttt cgt gac cgc tgt gta tcg gcg ggc att gat gtg gaa att att	624
Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile	
195 200 205	
ccg gga att ttg ccg gta tct aac ttt aaa cag gcg aag aaa ttt gcc	672
Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala	
210 215 220	
gat atg acc aac gtg cgt att ccg gcg tgg atg gcg caa atg ttc gac	720
Asp Met Thr Asn Val Arg Ile Pro Ala Trp Met Ala Gln Met Phe Asp	
225 230 235 240	
ggt ctg gat gat gat gcc gaa acc cgc aaa ctg gtt ggc gcg aat att	768
Gly Leu Asp Asp Asp Ala Glu Thr Arg Lys Leu Val Gly Ala Asn Ile	
245 250 255	
gcc atg gat atg gtg aag att tta agc cgt gaa gga gtg aaa gat ttc	816
Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe	
260 265 270	
cac ttc tat acg ctt aac cgt gct gaa atg agt tac gcg att tgc cat	864
His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His	
275 280 285	
acg ctg ggg gtt cga cct ggt tta taa	891
Thr Leu Gly Val Arg Pro Gly Leu	
290 295	

<210> 34

<211> 296

<212> PRT

<213> Escherichia coli

<400> 34

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Met Ser Phe Phe His Ala Ser Gln Arg Asp Ala Leu Asn Gln Ser Leu
 1             5             10             15

Ala Glu Val Gln Gly Gln Ile Asn Val Ser Phe Glu Phe Phe Pro Pro
      20             25             30

Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Asn Ser Ile Asp Arg Leu
      35             40             45

Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser
      50             55             60

Gly Glu Arg Asp Arg Thr His Ser Ile Ile Lys Gly Ile Lys Asp Arg
      65             70             75             80

Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Thr Pro
      85             90             95

Asp Glu Leu Arg Thr Ile Ala Arg Asp Tyr Trp Asn Asn Gly Ile Arg
      100            105            110

His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro
      115            120            125

Glu Met Tyr Ala Ser Asp Leu Val Thr Leu Leu Lys Glu Val Ala Asp
      130            135            140

Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys
      145            150            155            160

Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Asp Ala Gly
      165            170            175

Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu
      180            185            190

Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile
      195            200            205

Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala
      210            215            220

Asp Met Thr Asn Val Arg Ile Pro Ala Trp Met Ala Gln Met Phe Asp
      225            230            235            240

Gly Leu Asp Asp Asp Ala Glu Thr Arg Lys Leu Val Gly Ala Asn Ile
      245            250            255

Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe
      260            265            270

His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His
      275            280            285

Thr Leu Gly Val Arg Pro Gly Leu
      290            295

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<210> 35
 <211> 915
 <212> DNA
 <213> *Vibrio cholerae*

<220>
 <221> CDS
 <222> (1)..(912)
 <223> RVC06433

<400> 35
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 Val Thr Leu Gly His Arg Glu Tyr Lys Met Gly Tyr Thr His Ala Ser
 1 5 10 15

cat atc gat gca ttg aac caa aac att gcg gag ctt tcc gac atc aat 96
 His Ile Asp Ala Leu Asn Gln Asn Ile Ala Glu Leu Ser Asp Ile Asn
 20 25 30

gtt tcg ttt gag ttt ttt cca ccc agc tca cca caa atg gaa gaa acg 144
 Val Ser Phe Glu Phe Phe Pro Pro Ser Ser Pro Gln Met Glu Glu Thr
 35 40 45

ctt tgg gga tcg gta cac cgt ctg aaa aca ctc caa ccg aaa ttt gtt 192
 Leu Trp Gly Ser Val His Arg Leu Lys Thr Leu Gln Pro Lys Phe Val
 50 55 60

tcg gtc act tat ggt gca aac tct ggt gag cgt gac cgt act cac tcg 240
 Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu Arg Asp Arg Thr His Ser
 65 70 75 80

atc att aaa gcg atc aaa gat caa acc ggt tta att gcc gcg cca cac 288
 Ile Ile Lys Ala Ile Lys Asp Gln Thr Gly Leu Ile Ala Ala Pro His
 85 90 95

ctg act tgt atc gat gcc act cgt gat gaa ctg atc cag atc gcc gat 336
 Leu Thr Cys Ile Asp Ala Thr Arg Asp Glu Leu Ile Gln Ile Ala Asp
 100 105 110

gac tac tgg cat aac ggc atc cag aat att gtg gcg ctg cgt ggg gat 384
 Asp Tyr Trp His Asn Gly Ile Gln Asn Ile Val Ala Leu Arg Gly Asp
 115 120 125

atc ccg gct ggc ggt ggt aag cca gag atg tac gcc tcc gat cta gtg 432
 Ile Pro Ala Gly Gly Gly Lys Pro Glu Met Tyr Ala Ser Asp Leu Val
 130 135 140

acg ctg ctc aaa tca cgc cac gat ttt gat att tcc gtg gcc gcc ttc 480
 Thr Leu Leu Lys Ser Arg His Asp Phe Asp Ile Ser Val Ala Ala Phe
 145 150 155 160

cct gaa gtg cac cct gaa gcc aaa agc gcg caa gcg gac ctg ctc aat 528
 Pro Glu Val His Pro Glu Ala Lys Ser Ala Gln Ala Asp Leu Leu Asn
 165 170 175

tta aaa cgt aaa gtc gat gca ggt gcg aat cgt gcc atc acg cag ttt 576
 Leu Lys Arg Lys Val Asp Ala Gly Ala Asn Arg Ala Ile Thr Gln Phe
 180 185 190

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ttc ttt gat gta gaa agc tac ctg cgt ttt cgc gat cgc tgt gtg gcc 624
Phe Phe Asp Val Glu Ser Tyr Leu Arg Phe Arg Asp Arg Cys Val Ala
      195                      200                      205

gct ggg att gac gta gaa atc gtg cct ggc att ctg ccg gtt tct aac 672
Ala Gly Ile Asp Val Glu Ile Val Pro Gly Ile Leu Pro Val Ser Asn
      210                      215                      220

ttt aaa caa gcg tcg cgc ttc gct gcg caa aac aac gtc aaa gtt ccg 720
Phe Lys Gln Ala Ser Arg Phe Ala Ala Gln Asn Asn Val Lys Val Pro
      225                      230                      235                      240

aat tgg atg gtg aag cag ttt gaa gga tta gaa gac gat cca gtg act 768
Asn Trp Met Val Lys Gln Phe Glu Gly Leu Glu Asp Asp Pro Val Thr
      245                      250                      255

cgc cag ttg gta ggt gca agc caa gcc att gat atg gtg cgc gtg ctg 816
Arg Gln Leu Val Gly Ala Ser Gln Ala Ile Asp Met Val Arg Val Leu
      260                      265                      270

tgc cgt gaa ggg gtg aag gat ttc cac ttc tac acc cta aat cgt gcc 864
Cys Arg Glu Gly Val Lys Asp Phe His Phe Tyr Thr Leu Asn Arg Ala
      275                      280                      285

gaa atg act tac gcg tta tgc cac acc tta ggc gtt cgc cca caa gct 912
Glu Met Thr Tyr Ala Leu Cys His Thr Leu Gly Val Arg Pro Gln Ala
      290                      295                      300

taa 915

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<210> 36
<211> 304
<212> PRT
<213> Vibrio cholerae

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<400> 36
Val Thr Leu Gly His Arg Glu Tyr Lys Met Gly Tyr Thr His Ala Ser
  1                      5                      10                      15

His Ile Asp Ala Leu Asn Gln Asn Ile Ala Glu Leu Ser Asp Ile Asn
      20                      25                      30

Val Ser Phe Glu Phe Phe Pro Pro Ser Ser Pro Gln Met Glu Glu Thr
      35                      40                      45

Leu Trp Gly Ser Val His Arg Leu Lys Thr Leu Gln Pro Lys Phe Val
      50                      55                      60

Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu Arg Asp Arg Thr His Ser
      65                      70                      75                      80

Ile Ile Lys Ala Ile Lys Asp Gln Thr Gly Leu Ile Ala Ala Pro His
      85                      90                      95

Leu Thr Cys Ile Asp Ala Thr Arg Asp Glu Leu Ile Gln Ile Ala Asp
      100                      105                      110

Asp Tyr Trp His Asn Gly Ile Gln Asn Ile Val Ala Leu Arg Gly Asp

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115	120	125
Ile Pro Ala Gly Gly Gly Lys Pro Glu Met Tyr Ala Ser Asp Leu Val 130 135 140		
Thr Leu Leu Lys Ser Arg His Asp Phe Asp Ile Ser Val Ala Ala Phe 145 150 155 160		
Pro Glu Val His Pro Glu Ala Lys Ser Ala Gln Ala Asp Leu Leu Asn 165 170 175		
Leu Lys Arg Lys Val Asp Ala Gly Ala Asn Arg Ala Ile Thr Gln Phe 180 185 190		
Phe Phe Asp Val Glu Ser Tyr Leu Arg Phe Arg Asp Arg Cys Val Ala 195 200 205		
Ala Gly Ile Asp Val Glu Ile Val Pro Gly Ile Leu Pro Val Ser Asn 210 215 220		
Phe Lys Gln Ala Ser Arg Phe Ala Ala Gln Asn Asn Val Lys Val Pro 225 230 235 240		
Asn Trp Met Val Lys Gln Phe Glu Gly Leu Glu Asp Asp Pro Val Thr 245 250 255		
Arg Gln Leu Val Gly Ala Ser Gln Ala Ile Asp Met Val Arg Val Leu 260 265 270		
Cys Arg Glu Gly Val Lys Asp Phe His Phe Tyr Thr Leu Asn Arg Ala 275 280 285		
Glu Met Thr Tyr Ala Leu Cys His Thr Leu Gly Val Arg Pro Gln Ala 290 295 300		

<210> 37
 <211> 879
 <212> DNA
 <213> Haemophilus influenzae

<220>
 <221> CDS
 <222> (1)..(876)
 <223> RHI06620

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atg agc tac gcg aaa gaa att gat aca tta aat caa cat att gca gat Met Ser Tyr Ala Lys Glu Ile Asp Thr Leu Asn Gln His Ile Ala Asp 1 5 10 15	48
ttt aat aaa aaa att aat gtc tcc ttt gaa ttt ttt cca cct aaa aac Phe Asn Lys Lys Ile Asn Val Ser Phe Glu Phe Phe Pro Pro Lys Asn 20 25 30	96
gaa aaa atg gaa acc ctt cta tgg gat tca att cat cgt tta aaa gta Glu Lys Met Glu Thr Leu Leu Trp Asp Ser Ile His Arg Leu Lys Val	144

35	40	45	
tta aag cct aaa ttt gtg tca gtc act tac ggt gca aat tcg gga gaa Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu 50 55 60			192
cgt gac cgc act cac ggc att gtg aaa gcc att aaa caa gaa act ggc Arg Asp Arg Thr His Gly Ile Val Lys Ala Ile Lys Gln Glu Thr Gly 65 70 75 80			240
tta gaa gcc gca cca cat tta act gga att gat gcc aca cct gaa gaa Leu Glu Ala Ala Pro His Leu Thr Gly Ile Asp Ala Thr Pro Glu Glu 85 90 95			288
tta aaa caa att gcg aga gat tat tgg gat agt ggt att cgc cgt att Leu Lys Gln Ile Ala Arg Asp Tyr Trp Asp Ser Gly Ile Arg Arg Ile 100 105 110			336
gtt gcg tta cgc ggt gac gaa cct aaa ggt tac gcg aaa aaa cca ttt Val Ala Leu Arg Gly Asp Glu Pro Lys Gly Tyr Ala Lys Lys Pro Phe 115 120 125			384
tat gcg tca gat ctt gtg gaa tta ctc cgt tct gtc gct gat ttt gat Tyr Ala Ser Asp Leu Val Glu Leu Leu Arg Ser Val Ala Asp Phe Asp 130 135 140			432
att tct gta gcc gct tat ccc gaa gtt cat cca gaa gca aaa tcc gca Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys Ser Ala 145 150 155 160			480
caa gca gac tta att aat tta aaa cgt aaa att gat gca ggt gca aac Gln Ala Asp Leu Ile Asn Leu Lys Arg Lys Ile Asp Ala Gly Ala Asn 165 170 175			528
cac gtc att aca caa ttt ttc ttt gat att gaa aac tac cta cgt ttt His Val Ile Thr Gln Phe Phe Phe Asp Ile Glu Asn Tyr Leu Arg Phe 180 185 190			576
cgt gat cgt tgt gca tca att ggt att gat act gaa atc gta ccc ggt Arg Asp Arg Cys Ala Ser Ile Gly Ile Asp Thr Glu Ile Val Pro Gly 195 200 205			624
att tta cct gtt act aat ttt aaa caa ctc caa aaa atg gca tca ttc Ile Leu Pro Val Thr Asn Phe Lys Gln Leu Gln Lys Met Ala Ser Phe 210 215 220			672
act aat gtg aaa att cca gcg tgg tta gtt aaa gcc tat gat ggt ttg Thr Asn Val Lys Ile Pro Ala Trp Leu Val Lys Ala Tyr Asp Gly Leu 225 230 235 240			720
gat aat gat cca act aca cgt aat ctt gtg gca gca agt gtt gca atg Asp Asn Asp Pro Thr Thr Arg Asn Leu Val Ala Ala Ser Val Ala Met 245 250 255			768
gat atg gta aaa att tta tct cgc gaa ggc gtg aat gac ttc cac ttt Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Asn Asp Phe His Phe 260 265 270			816
tat aca tta aat cgt agt gaa tta act tat gct atc tgt cat atg tta Tyr Thr Leu Asn Arg Ser Glu Leu Thr Tyr Ala Ile Cys His Met Leu			864

275 280 285
 ggt gta aga cct taa
 Gly Val Arg Pro
 290

879

<210> 38
 <211> 292
 <212> PRT
 <213> Haemophilus influenzae

<400> 38
 Met Ser Tyr Ala Lys Glu Ile Asp Thr Leu Asn Gln His Ile Ala Asp
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Phe Asn Lys Lys Ile Asn Val Ser Phe Glu Phe Phe Pro Pro Lys Asn
 20 25 30

Glu Lys Met Glu Thr Leu Leu Trp Asp Ser Ile His Arg Leu Lys Val
 35 40 45

Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu
 50 55 60

Arg Asp Arg Thr His Gly Ile Val Lys Ala Ile Lys Gln Glu Thr Gly
 65 70 75 80

Leu Glu Ala Ala Pro His Leu Thr Gly Ile Asp Ala Thr Pro Glu Glu
 85 90 95

Leu Lys Gln Ile Ala Arg Asp Tyr Trp Asp Ser Gly Ile Arg Arg Ile
 100 105 110

Val Ala Leu Arg Gly Asp Glu Pro Lys Gly Tyr Ala Lys Lys Pro Phe
 115 120 125

Tyr Ala Ser Asp Leu Val Glu Leu Leu Arg Ser Val Ala Asp Phe Asp
 130 135 140

Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys Ser Ala
 145 150 155 160

Gln Ala Asp Leu Ile Asn Leu Lys Arg Lys Ile Asp Ala Gly Ala Asn
 165 170 175

His Val Ile Thr Gln Phe Phe Phe Asp Ile Glu Asn Tyr Leu Arg Phe
 180 185 190

Arg Asp Arg Cys Ala Ser Ile Gly Ile Asp Thr Glu Ile Val Pro Gly
 195 200 205

Ile Leu Pro Val Thr Asn Phe Lys Gln Leu Gln Lys Met Ala Ser Phe
 210 215 220

Thr Asn Val Lys Ile Pro Ala Trp Leu Val Lys Ala Tyr Asp Gly Leu
 225 230 235 240

Asp Asn Asp Pro Thr Thr Arg Asn Leu Val Ala Ala Ser Val Ala Met

	245		250		255	
Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Asn Asp Phe His Phe						
	260		265		270	
Tyr Thr Leu Asn Arg Ser Glu Leu Thr Tyr Ala Ile Cys His Met Leu						
	275		280		285	
Gly Val Arg Pro						
	290					

<210> 39
 <211> 945
 <212> DNA
 <213> *Caulobacter crescentus*

<220>
 <221> CDS
 <222> (1) .. (942)
 <223> RCO02274

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Gly Glu Arg Thr Gly Arg Pro Arg Val Ser Phe Glu Phe Phe Pro Pro	
20 25 30	
aag act ccg cag atg gaa gag agc ctg tgg cag gcg atc aca cgc ctg	144
Lys Thr Pro Gln Met Glu Glu Ser Leu Trp Gln Ala Ile Thr Arg Leu	
35 40 45	
gcg ccg ctg gat ccg gcc ttc gtc tcg gtg acc tat ggc gcg ggc ggc	192
Ala Pro Leu Asp Pro Ala Phe Val Ser Val Thr Tyr Gly Ala Gly Gly	
50 55 60	
tcc acc cgc gag cgc acc cac cgc acc gtc aag cgg atc ctg gac gag	240
Ser Thr Arg Glu Arg Thr His Arg Thr Val Lys Arg Ile Leu Asp Glu	
65 70 75 80	
acc agc ctc aag ccc gcc gcg cac ctg acc tgc gtc ggc gcc agt cgc	288
Thr Ser Leu Lys Pro Ala Ala His Leu Thr Cys Val Gly Ala Ser Arg	
85 90 95	
gaa gag gtc gat gag gtc att cgc gag tac tgg gag acc ggg gtc cgt	336
Glu Glu Val Asp Glu Val Ile Arg Glu Tyr Trp Glu Thr Gly Val Arg	
100 105 110	
cac atc gtt tcg ctg cgg ggc gat ccg ccg ccc ggc gag ggc ggc atc	384
His Ile Val Ser Leu Arg Gly Asp Pro Pro Pro Gly Glu Gly Gly Ile	
115 120 125	
ggc ggg gtc tat gtg ccg cgc gcc gac ggc tac gcc aac gcc aca gag	432
Gly Gly Val Tyr Val Pro Arg Ala Asp Gly Tyr Ala Asn Ala Thr Glu	
130 135 140	
ttg acc aag gcc gtg cgc gcg atc gcg ccg ttc gag gtg ctg gtc ggg	480

Leu Thr Lys Ala Val Arg Ala Ile Ala Pro Phe Glu Val Leu Val Gly
 145 150 155 160
 gtc tat ccc gag aag cat ccc gag agc ccc tcg ttg gag cac gac atc 528
 Val Tyr Pro Glu Lys His Pro Glu Ser Pro Ser Leu Glu His Asp Ile
 165 170 175
 gac gtc ttg aag cag aag gtc gac gcc ggc gcg acg ctg ggg atc agc 576
 Asp Val Leu Lys Gln Lys Val Asp Ala Gly Ala Thr Leu Gly Ile Ser
 180 185 190
 cag ttc ttc ttc gac ctc gac gcc ttc ctg cgc ttc gtc gac aag gtg 624
 Gln Phe Phe Phe Asp Leu Asp Ala Phe Leu Arg Phe Val Asp Lys Val
 195 200 205
 cgc gcg gcg ggc atc acc att ccg atc gtg ccg ggg atc atg ccg gtg 672
 Arg Ala Ala Gly Ile Thr Ile Pro Ile Val Pro Gly Ile Met Pro Val
 210 215 220
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 Thr Asn Phe Ala Gly Leu Lys Lys Met Ala Ala Ala Cys Gln Thr Ala
 225 230 235 240
 atc ccg tcc tgg ctg ggg aac ctg ttc gac ggg ctg gag aac gac gcg 768
 Ile Pro Ser Trp Leu Gly Asn Leu Phe Asp Gly Leu Glu Asn Asp Ala
 245 250 255
 gag acc cgc cgc ctg atc gcc tgt tcg gtg gcc gcc gag atg tgc gcc 816
 Glu Thr Arg Arg Leu Ile Ala Cys Ser Val Ala Ala Glu Met Cys Ala
 260 265 270
 aag ctg cag gaa cag ggt ttc gag gac ttc cac ttc tac acc ctg aac 864
 Lys Leu Gln Glu Gln Gly Phe Glu Asp Phe His Phe Tyr Thr Leu Asn
 275 280 285
 cgg gcc gat ctc gtt tac gcc atc tgc cgt gtg ctg ggc gtg cgc gag 912
 Arg Ala Asp Leu Val Tyr Ala Ile Cys Arg Val Leu Gly Val Arg Glu
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 Ile Ser Pro Ala Ala Ser Glu Val Ala Ala
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<210> 40

<211> 314

<212> PRT

<213> *Caulobacter crescentus*

<400> 40

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 Lys Thr Pro Gln Met Glu Glu Ser Leu Trp Gln Ala Ile Thr Arg Leu
 35 40 45
 Ala Pro Leu Asp Pro Ala Phe Val Ser Val Thr Tyr Gly Ala Gly Gly

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Thr	Ser	Leu	Lys	Pro 85	Ala	Ala	His	Leu	Thr 90	Cys	Val	Gly	Ala	Ser 95	Arg			
Glu	Glu	Val	Asp 100	Glu	Val	Ile	Arg	Glu 105	Tyr	Trp	Glu	Thr	Gly 110	Val	Arg			
His	Ile	Val 115	Ser	Leu	Arg	Gly	Asp 120	Pro	Pro	Pro	Gly	Glu 125	Gly	Gly	Ile			
Gly 130	Gly	Val	Tyr	Val	Pro	Arg 135	Ala	Asp	Gly	Tyr	Ala 140	Asn	Ala	Thr	Glu			
Leu 145	Thr	Lys	Ala	Val	Arg 150	Ala	Ile	Ala	Pro	Phe 155	Glu	Val	Leu	Val	Gly 160			
Val	Tyr	Pro	Glu	Lys 165	His	Pro	Glu	Ser	Pro 170	Ser	Leu	Glu	His	Asp 175	Ile			
Asp	Val	Leu	Lys 180	Gln	Lys	Val	Asp	Ala 185	Gly	Ala	Thr	Leu	Gly 190	Ile	Ser			
Gln	Phe	Phe 195	Phe	Asp	Leu	Asp	Ala 200	Phe	Leu	Arg	Phe	Val 205	Asp	Lys	Val			
Arg 210	Ala	Ala	Gly	Ile	Thr	Ile 215	Pro	Ile	Val	Pro	Gly 220	Ile	Met	Pro	Val			
Thr 225	Asn	Phe	Ala	Gly 230	Leu	Lys	Lys	Met	Ala 235	Ala	Ala	Cys	Gln	Thr	Ala 240			
Ile	Pro	Ser	Trp 245	Leu	Gly	Asn	Leu	Phe	Asp 250	Gly	Leu	Glu	Asn	Asp 255	Ala			
Glu	Thr	Arg	Arg 260	Leu	Ile	Ala	Cys	Ser	Val 265	Ala	Ala	Glu	Met	Cys	Ala			
Lys	Leu	Gln 275	Glu	Gln	Gly	Phe	Glu 280	Asp	Phe	His	Phe	Tyr 285	Thr	Leu	Asn			
Arg 290	Ala	Asp	Leu	Val	Tyr 295	Ala	Ile	Cys	Arg	Val	Leu 300	Gly	Val	Arg	Glu			
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<210> 41
<211> 885
<212> DNA
<213> Actinobacillus actinomycetemcomitans
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<223> RAB00260

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tta aac ggc aaa att aat gtc tct ttt gaa ttt ttc ccg ccg aaa agt	96
Leu Asn Gly Lys Ile Asn Val Ser Phe Glu Phe Phe Pro Pro Lys Ser	
20 25 30	
gaa aaa atg gaa aat ctt ctg tgg gaa tcc atc cat cgc tta aaa gtg	144
Glu Lys Met Glu Asn Leu Leu Trp Glu Ser Ile His Arg Leu Lys Val	
35 40 45	
cta aaa ccg aaa ttt gta tcc gtg act tac ggc gcc aat tcc ggc gag	192
Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu	
50 55 60	
cgt gaa cgc act cac ggg gtg gtg aaa cgc att aag cag gaa acc ggt	240
Arg Glu Arg Thr His Gly Val Val Lys Arg Ile Lys Gln Glu Thr Gly	
65 70 75 80	
ctg gaa gct gcg ccg cat tta acc ggt att gac gct acc tcg gac gaa	288
Leu Glu Ala Ala Pro His Leu Thr Gly Ile Asp Ala Thr Ser Asp Glu	
85 90 95	
ttg cgt cgc att gcc aaa ggt tat tgg gat agc ggc att cgt cgc att	336
Leu Arg Arg Ile Ala Lys Gly Tyr Trp Asp Ser Gly Ile Arg Arg Ile	
100 105 110	
gtg gca ctg cgc ggt gac gag ccg aaa ggc tac gag aaa aaa cca ttt	384
Val Ala Leu Arg Gly Asp Glu Pro Lys Gly Tyr Glu Lys Lys Pro Phe	
115 120 125	
tat gcc gcc gat tta gta gca tta tta cgt gac gta tca gat ttt gat	432
Tyr Ala Ala Asp Leu Val Ala Leu Leu Arg Asp Val Ser Asp Phe Asp	
130 135 140	
att tcc gtg gcg gca tac cct gag gtt cat ccg gaa gcc aaa tcg gcg	480
Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys Ser Ala	
145 150 155 160	
caa gcg gat tta att aat tta aaa cgt aaa att gat gcc ggt gcc aat	528
Gln Ala Asp Leu Ile Asn Leu Lys Arg Lys Ile Asp Ala Gly Ala Asn	
165 170 175	
cat gtg atc aca caa ttc ttt ttc gat att gac agc tat ctg cgg ttc	576
His Val Ile Thr Gln Phe Phe Phe Asp Ile Asp Ser Tyr Leu Arg Phe	
180 185 190	
cgc gat cgc tgc gcg tct atc ggt att gat gca gaa atc gtg ccg ggg	624
Arg Asp Arg Cys Ala Ser Ile Gly Ile Asp Ala Glu Ile Val Pro Gly	
195 200 205	
att ctg ccg gtg acc aac ttc aaa caa tta caa aaa atg gca gca atc	672
Ile Leu Pro Val Thr Asn Phe Lys Gln Leu Gln Lys Met Ala Ala Ile	
210 215 220	
act aat gtg aaa att cca gct tgg atg agc aaa atg tat gaa ggc ttg	720

Thr Asn Val Lys Ile Pro Ala Trp Met Ser Lys Met Tyr Glu Gly Leu
 225 230 235 240
 gat gat gac caa acc acc cgc aat ctg gtg gcg gcg agc atc gcc atg 768
 Asp Asp Asp Gln Thr Thr Arg Asn Leu Val Ala Ala Ser Ile Ala Met
 245 250 255
 gac atg gtg cgt gta ctg tcc cgc gaa ggg gta aaa gac ttt cat ttc 816
 Asp Met Val Arg Val Leu Ser Arg Glu Gly Val Lys Asp Phe His Phe
 260 265 270
 tac acc ctg aat cgc agt gaa ctc acc tat gct att tgc cac acg tta 864
 Tyr Thr Leu Asn Arg Ser Glu Leu Thr Tyr Ala Ile Cys His Thr Leu
 275 280 285
 ggc att cgt ccg agt ttg taa 885
 Gly Ile Arg Pro Ser Leu
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 <210> 42
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 <213> Actinobacillus actinomycetemcomitans
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 35 40 45
 Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu
 50 55 60
 Arg Glu Arg Thr His Gly Val Val Lys Arg Ile Lys Gln Glu Thr Gly
 65 70 75 80
 Leu Glu Ala Ala Pro His Leu Thr Gly Ile Asp Ala Thr Ser Asp Glu
 85 90 95
 Leu Arg Arg Ile Ala Lys Gly Tyr Trp Asp Ser Gly Ile Arg Arg Ile
 100 105 110
 Val Ala Leu Arg Gly Asp Glu Pro Lys Gly Tyr Glu Lys Lys Pro Phe
 115 120 125
 Tyr Ala Ala Asp Leu Val Ala Leu Leu Arg Asp Val Ser Asp Phe Asp
 130 135 140
 Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys Ser Ala
 145 150 155 160
 Gln Ala Asp Leu Ile Asn Leu Lys Arg Lys Ile Asp Ala Gly Ala Asn
 165 170 175
 His Val Ile Thr Gln Phe Phe Phe Asp Ile Asp Ser Tyr Leu Arg Phe

180					185					190						
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210					215					220						
Thr	Asn	Val	Lys	Ile	Pro	Ala	Trp	Met	Ser	Lys	Met	Tyr	Glu	Gly	Leu	
225					230					235					240	
Asp	Asp	Asp	Gln	Thr	Thr	Arg	Asn	Leu	Val	Ala	Ala	Ser	Ile	Ala	Met	
245					250					255						
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260					265					270						
Tyr	Thr	Leu	Asn	Arg	Ser	Glu	Leu	Thr	Tyr	Ala	Ile	Cys	His	Thr	Leu	
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<220>
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 <222> (1)..(864)
 <223> RRC03981

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gac gcc tcg ttc cgg ctg tgg gag acg gcg cag gtt ctg gcg ccg ctc	96	
Asp Ala Ser Phe Arg Leu Trp Glu Thr Ala Gln Val Leu Ala Pro Leu		
20 25 30		
aag ccc ggc ttc gtc tcg gtc acc tat ggc gcg ggc ggc acc acc cgc	144	
Lys Pro Gly Phe Val Ser Val Thr Tyr Gly Ala Gly Gly Thr Thr Arg		
35 40 45		
aag ctg acg cat gag gcc gtg gcg gcg atc cac aag aat tac ggc ctg	192	
Lys Leu Thr His Glu Ala Val Ala Ala Ile His Lys Asn Tyr Gly Leu		
50 55 60		
aac gtc gcc gcg cat ctg acc tgc gtc gat gcg acc cgg gcc gaa acg	240	
Asn Val Ala Ala His Leu Thr Cys Val Asp Ala Thr Arg Ala Glu Thr		
65 70 75 80		
caa gag atc atc gac gcc tat gcc gag gct ggc gtc acc gag att gtc	288	
Gln Glu Ile Ile Asp Ala Tyr Ala Glu Ala Gly Val Thr Glu Ile Val		
85 90 95		
gcg ctg cgc ggt gat ccg ccg aaa ggc gcc gcc cgc ttc acg ccg cat	336	

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Pro	Asp	Gly	Phe	Ala	Ser	Ser	Val	Asp	Leu	Ile	Glu	Trp	Leu	Ala	Arg		
		115					120				125						
gac	ggc	cgc	ttc	acg	ctg	cgc	tgc	ggc	gcc	tat	ccg	gaa	ccg	cat	ccg	432	
Asp	Gly	Arg	Phe	Thr	Leu	Arg	Cys	Gly	Ala	Tyr	Pro	Glu	Pro	His	Pro		
	130					135					140						
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Glu	Ala	Ala	Asp	Thr	Leu	Ala	Asp	Val	Arg	Trp	Leu	Lys	Arg	Lys	Cys		
145					150				155						160		
gag	gcg	ggg	gcg	acc	tcg	gcg	atc	acg	caa	ttc	ttc	ttt	gaa	gcc	gag	528	
Glu	Ala	Gly	Ala	Thr	Ser	Ala	Ile	Thr	Gln	Phe	Phe	Phe	Glu	Ala	Glu		
			165					170					175				
acc	ttc	ttc	cgc	ttc	cgc	gac	gcc	tgc	gtg	aag	gaa	ggg	atc	acc	gcc	576	
Thr	Phe	Phe	Arg	Phe	Arg	Asp	Ala	Cys	Val	Lys	Glu	Gly	Ile	Thr	Ala		
			180					185					190				
aag	atc	atc	ccg	ggc	atc	ctg	ccg	atc	cag	tcc	tgg	aaa	ggc	gcc	aag	624	
Lys	Ile	Ile	Pro	Gly	Ile	Leu	Pro	Ile	Gln	Ser	Trp	Lys	Gly	Ala	Lys		
	195					200					205						
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Ser	Phe	Ala	Gln	Arg	Cys	Gly	Thr	Ser	Ile	Pro	Thr	Trp	Val	Glu	Glu		
	210				215					220							
gcc	ttt	gac	cat	gcg	atc	cgc	gac	gac	cgc	gaa	cag	ctg	ctg	gcc	acg	720	
Ala	Phe	Asp	His	Ala	Ile	Arg	Asp	Asp	Arg	Glu	Gln	Leu	Leu	Ala	Thr		
225				230					235						240		
gcg	ctg	tgc	acg	gag	ctc	tgc	gac	aac	ctg	atc	gcg	ggc	ggg	gtg	gag	768	
Ala	Leu	Cys	Thr	Glu	Leu	Cys	Asp	Asn	Leu	Ile	Ala	Gly	Gly	Val	Glu		
			245					250					255				
gat	ctg	cat	ttc	tac	acg	ctg	aac	cgg	ccg	cag	atg	acc	cgc	gat	gtc	816	
Asp	Leu	His	Phe	Tyr	Thr	Leu	Asn	Arg	Pro	Gln	Met	Thr	Arg	Asp	Val		
		260					265					270					
tgc	cat	gcg	ctg	ggc	gtc	aac	ccg	ggt	gtg	gtg	ctg	gaa	aac	gtc	gcc	864	
Cys	His	Ala	Leu	Gly	Val	Asn	Pro	Gly	Val	Val	Leu	Glu	Asn	Val	Ala		
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<210> 44

<211> 288

<212> PRT

<213> Rhodobacter

<400> 44

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20					25					30					
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Lys	Leu	Thr	His	Glu	Ala	Val	Ala	Ala	Ile	His	Lys	Asn	Tyr	Gly	Leu
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Asn	Val	Ala	Ala	His	Leu	Thr	Cys	Val	Asp	Ala	Thr	Arg	Ala	Glu	Thr
	65					70					75				80
Gln	Glu	Ile	Ile	Asp	Ala	Tyr	Ala	Glu	Ala	Gly	Val	Thr	Glu	Ile	Val
				85					90					95	
Ala	Leu	Arg	Gly	Asp	Pro	Pro	Lys	Gly	Ala	Ala	Arg	Phe	Thr	Pro	His
			100					105					110		
Pro	Asp	Gly	Phe	Ala	Ser	Ser	Val	Asp	Leu	Ile	Glu	Trp	Leu	Ala	Arg
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Asp	Gly	Arg	Phe	Thr	Leu	Arg	Cys	Gly	Ala	Tyr	Pro	Glu	Pro	His	Pro
	130					135					140				
Glu	Ala	Ala	Asp	Thr	Leu	Ala	Asp	Val	Arg	Trp	Leu	Lys	Arg	Lys	Cys
	145					150					155				160
Glu	Ala	Gly	Ala	Thr	Ser	Ala	Ile	Thr	Gln	Phe	Phe	Phe	Glu	Ala	Glu
				165					170					175	
Thr	Phe	Phe	Arg	Phe	Arg	Asp	Ala	Cys	Val	Lys	Glu	Gly	Ile	Thr	Ala
			180					185					190		
Lys	Ile	Ile	Pro	Gly	Ile	Leu	Pro	Ile	Gln	Ser	Trp	Lys	Gly	Ala	Lys
		195					200					205			
Ser	Phe	Ala	Gln	Arg	Cys	Gly	Thr	Ser	Ile	Pro	Thr	Trp	Val	Glu	Glu
	210					215					220				
Ala	Phe	Asp	His	Ala	Ile	Arg	Asp	Asp	Arg	Glu	Gln	Leu	Leu	Ala	Thr
	225					230					235				240
Ala	Leu	Cys	Thr	Glu	Leu	Cys	Asp	Asn	Leu	Ile	Ala	Gly	Gly	Val	Glu
				245					250					255	
Asp	Leu	His	Phe	Tyr	Thr	Leu	Asn	Arg	Pro	Gln	Met	Thr	Arg	Asp	Val
		260						265					270		
Cys	His	Ala	Leu	Gly	Val	Asn	Pro	Gly	Val	Val	Leu	Glu	Asn	Val	Ala
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<211> 879

<212> DNA

<213> Neisseria meningitidis ser. A

<220>

<221> CDS

<222> (1)..(876)

<223> RNM00812

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ttg aaa ggc gac atc aac gtt tcg ttt gaa ttt ttt cca ccg aaa aac	96
Leu Lys Gly Asp Ile Asn Val Ser Phe Glu Phe Phe Pro Pro Lys Asn	
20 25 30	
gag caa atg gaa acg atg ctg tgg gat tcc atc cac cgt ctg caa acc	144
Glu Gln Met Glu Thr Met Leu Trp Asp Ser Ile His Arg Leu Gln Thr	
35 40 45	
ctg cat ccc aag ttc gta tcc gta acc tac ggc gca aac tcc ggc gaa	192
Leu His Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu	
50 55 60	
cgc gac cgc acg cac ggc atc gtc aaa cgc atc aaa cag gaa acc ggc	240
Arg Asp Arg Thr His Gly Ile Val Lys Arg Ile Lys Gln Glu Thr Gly	
65 70 75 80	
ttg gaa gca gca ccg cac ctg acc ggc atc gac gca tcc ccc gac gaa	288
Leu Glu Ala Ala Pro His Leu Thr Gly Ile Asp Ala Ser Pro Asp Glu	
85 90 95	
ttg cgc caa atc gcc aaa gac tat tgg gac agc ggc atc cgc cgc att	336
Leu Arg Gln Ile Ala Lys Asp Tyr Trp Asp Ser Gly Ile Arg Arg Ile	
100 105 110	
gtc gcc ctg cgt ggc gac gag ccg ccc ggt tat gag aaa aaa ccg ttt	384
Val Ala Leu Arg Gly Asp Glu Pro Pro Gly Tyr Glu Lys Lys Pro Phe	
115 120 125	
tac gcc gaa gac ttg gtt aag cta tta cgc tcc gtc gcc gac ttc gac	432
Tyr Ala Glu Asp Leu Val Lys Leu Leu Arg Ser Val Ala Asp Phe Asp	
130 135 140	
atc tct gtg gcg gca tat ccc gaa gtg cat ccc gaa gcc aaa tcc gca	480
Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys Ser Ala	
145 150 155 160	
caa gcc gat ctg att aat ctg aag cgc aaa atc gat gcg ggt gca aac	528
Gln Ala Asp Leu Ile Asn Leu Lys Arg Lys Ile Asp Ala Gly Ala Asn	
165 170 175	
cac gtc atc acc caa ttt ttc ttt gac gta gaa cgc tac ctg cgc ttc	576
His Val Ile Thr Gln Phe Phe Phe Asp Val Glu Arg Tyr Leu Arg Phe	
180 185 190	
cgc gac cgc tgc gtg atg ttg ggt atc gat gtg gaa atc gtc cct ggt	624
Arg Asp Arg Cys Val Met Leu Gly Ile Asp Val Glu Ile Val Pro Gly	
195 200 205	
att ttg cct gtt acc aac ttc aag cag ctc ggc aaa atg gcg caa gta	672
Ile Leu Pro Val Thr Asn Phe Lys Gln Leu Gly Lys Met Ala Gln Val	
210 215 220	

acc aac gtc aaa atc cca agc tgg ctg tcg caa atg tat gaa ggt ttg 720
 Thr Asn Val Lys Ile Pro Ser Trp Leu Ser Gln Met Tyr Glu Gly Leu
 225 230 235 240

gac gac gac caa ggc acg cgc aac ctc gtc gcc gcc agt atc gcc atc 768
 Asp Asp Asp Gln Gly Thr Arg Asn Leu Val Ala Ala Ser Ile Ala Ile
 245 250 255

gat atg gtc aaa gtc ctg tcc cgc gaa ggc gtg aaa gat ttc cac ttc 816
 Asp Met Val Lys Val Leu Ser Arg Glu Gly Val Lys Asp Phe His Phe
 260 265 270

tac acg ctc aac cgc agc gag ctg act tac gcc atc tgc cat att tta 864
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ggc gtg cgc cct taa 879
 Gly Val Arg Pro
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<210> 46

<211> 292

<212> PRT

<213> Neisseria meningitidis ser. A

<400> 46

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Glu Gln Met Glu Thr Met Leu Trp Asp Ser Ile His Arg Leu Gln Thr
 35 40 45

Leu His Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu
 50 55 60

Arg Asp Arg Thr His Gly Ile Val Lys Arg Ile Lys Gln Glu Thr Gly
 65 70 75 80

Leu Glu Ala Ala Pro His Leu Thr Gly Ile Asp Ala Ser Pro Asp Glu
 85 90 95

Leu Arg Gln Ile Ala Lys Asp Tyr Trp Asp Ser Gly Ile Arg Arg Ile
 100 105 110

Val Ala Leu Arg Gly Asp Glu Pro Pro Gly Tyr Glu Lys Lys Pro Phe
 115 120 125

Tyr Ala Glu Asp Leu Val Lys Leu Leu Arg Ser Val Ala Asp Phe Asp
 130 135 140

Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys Ser Ala
 145 150 155 160

Gln Ala Asp Leu Ile Asn Leu Lys Arg Lys Ile Asp Ala Gly Ala Asn
 165 170 175

His Val Ile Thr Gln Phe Phe Phe Asp Val Glu Arg Tyr Leu Arg Phe
180 185 190

Arg Asp Arg Cys Val Met Leu Gly Ile Asp Val Glu Ile Val Pro Gly
195 200 205

Ile Leu Pro Val Thr Asn Phe Lys Gln Leu Gly Lys Met Ala Gln Val
210 215 220

Thr Asn Val Lys Ile Pro Ser Trp Leu Ser Gln Met Tyr Glu Gly Leu
225 230 235 240

Asp Asp Asp Gln Gly Thr Arg Asn Leu Val Ala Ala Ser Ile Ala Ile
245 250 255

Asp Met Val Lys Val Leu Ser Arg Glu Gly Val Lys Asp Phe His Phe
260 265 270

Tyr Thr Leu Asn Arg Ser Glu Leu Thr Tyr Ala Ile Cys His Ile Leu
275 280 285

Gly Val Arg Pro
290

<210> 47

<211> 849

<212> DNA

<213> Campylobacter jejuni

<220>

<221> CDS

<222> (1)..(846)

<223> RCJ02911

<400> 47

atg tgt agt ttt tct ttt gaa gtt ttt cca cca aga aag gat gaa aat 48
Met Cys Ser Phe Ser Phe Glu Val Phe Pro Pro Arg Lys Asp Glu Asn
1 5 10 15

atc aaa aat ctt cat gct atc tta gat gat tta ggg caa tta agc cct 96
Ile Lys Asn Leu His Ala Ile Leu Asp Asp Leu Gly Gln Leu Ser Pro
20 25 30

aat ttt atc agc gta acc ttt gga gct gga ggc tct att aac tca caa 144
Asn Phe Ile Ser Val Thr Phe Gly Ala Gly Gly Ser Ile Asn Ser Gln
35 40 45

aat act tta gaa gtt gca agc tta atc cag gaa gaa tat caa att cct 192
Asn Thr Leu Glu Val Ala Ser Leu Ile Gln Glu Glu Tyr Gln Ile Pro
50 55 60

agc ata gta cat tta cct tgc atc cat tct agt aaa gaa aaa atc act 240
Ser Ile Val His Leu Pro Cys Ile His Ser Ser Lys Glu Lys Ile Thr
65 70 75 80

cag ata ctt caa aaa tgc aaa gaa aaa aat ctt aat caa att ctt gcc 288
Gln Ile Leu Gln Lys Cys Lys Glu Lys Asn Leu Asn Gln Ile Leu Ala

85										90					95					
cta	aga	ggc	gat	ata	tgt	gaa	aat	tta	aaa	aaa	agc	aaa	gat	ttt	tct	336				
Leu	Arg	Gly	Asp	Ile	Cys	Glu	Asn	Leu	Lys	Lys	Ser	Lys	Asp	Phe	Ser					
100					105					110										
tat	gct	agt	gat	tta	att	tct	ttt	ata	aaa	aaa	caa	gaa	tac	ttt	gaa	384				
Tyr	Ala	Ser	Asp	Leu	Ile	Ser	Phe	Ile	Lys	Lys	Gln	Glu	Tyr	Phe	Glu					
115					120					125										
att	tat	gcc	gca	tgc	tat	ccc	gaa	aaa	cat	aat	gaa	tct	aaa	aat	ttc	432				
Ile	Tyr	Ala	Ala	Cys	Tyr	Pro	Glu	Lys	His	Asn	Glu	Ser	Lys	Asn	Phe					
130					135					140										
atc	gag	gat	ata	cac	cat	ctt	aaa	act	aag	gta	aat	gca	gga	aca	gat	480				
Ile	Glu	Asp	Ile	His	His	Leu	Lys	Thr	Lys	Val	Asn	Ala	Gly	Thr	Asp					
145					150					155					160					
aag	ctc	att	act	caa	ctt	ttt	tac	gat	aat	gaa	gat	ttt	tat	act	ttt	528				
Lys	Leu	Ile	Thr	Gln	Leu	Phe	Tyr	Asp	Asn	Glu	Asp	Phe	Tyr	Thr	Phe					
165					170					175										
aaa	caa	aat	tgt	gct	tta	gca	gat	att	gac	ata	cct	att	tac	gca	ggt	576				
Lys	Gln	Asn	Cys	Ala	Leu	Ala	Asp	Ile	Asp	Ile	Pro	Ile	Tyr	Ala	Gly					
180					185					190										
att	atg	cct	att	act	aac	aaa	aga	cag	gtt	tta	aaa	att	tct	caa	ctt	624				
Ile	Met	Pro	Ile	Thr	Asn	Lys	Arg	Gln	Val	Leu	Lys	Ile	Ser	Gln	Leu					
195					200					205										
tgc	gga	gct	aaa	atc	cct	cct	aaa	ttt	gtt	aaa	att	tta	gaa	aaa	tat	672				
Cys	Gly	Ala	Lys	Ile	Pro	Pro	Lys	Phe	Val	Lys	Ile	Leu	Glu	Lys	Tyr					
210					215					220										
gaa	aat	aat	act	ttg	got	tta	gaa	gat	gca	ggt	atc	gcg	tat	gct	tgc	720				
Glu	Asn	Asn	Thr	Leu	Ala	Leu	Glu	Asp	Ala	Gly	Ile	Ala	Tyr	Ala	Cys					
225					230					235					240					
gat	caa	att	gtc	gat	tta	atc	aca	agt	ggt	gta	gat	gga	att	cat	ctt	768				
Asp	Gln	Ile	Val	Asp	Leu	Ile	Thr	Ser	Gly	Val	Asp	Gly	Ile	His	Leu					
245					250					255										
tat	act	atg	aat	aaa	tcc	aaa	gcg	gct	att	aaa	att	tat	gaa	gct	gta	816				
Tyr	Thr	Met	Asn	Lys	Ser	Lys	Ala	Ala	Ile	Lys	Ile	Tyr	Glu	Ala	Val					
260					265					270										
aag	cat	ttg	ctt	aaa	gaa	gag	ctt	cat	gct	tag						849				
Lys	His	Leu	Leu	Lys	Glu	Glu	Leu	His	Ala											
275					280															

<210> 48

<211> 282

<212> PRT

<213> Campylobacter jejuni

<400> 48

Met	Cys	Ser	Phe	Ser	Phe	Glu	Val	Phe	Pro	Pro	Arg	Lys	Asp	Glu	Asn
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Ile Lys Asn Leu His Ala Ile Leu Asp Asp Leu Gly Gln Leu Ser Pro
 20 25 30
 Asn Phe Ile Ser Val Thr Phe Gly Ala Gly Gly Ser Ile Asn Ser Gln
 35 40 45
 Asn Thr Leu Glu Val Ala Ser Leu Ile Gln Glu Glu Tyr Gln Ile Pro
 50 55 60
 Ser Ile Val His Leu Pro Cys Ile His Ser Ser Lys Glu Lys Ile Thr
 65 70 75 80
 Gln Ile Leu Gln Lys Cys Lys Glu Lys Asn Leu Asn Gln Ile Leu Ala
 85 90 95
 Leu Arg Gly Asp Ile Cys Glu Asn Leu Lys Lys Ser Lys Asp Phe Ser
 100 105 110
 Tyr Ala Ser Asp Leu Ile Ser Phe Ile Lys Lys Gln Glu Tyr Phe Glu
 115 120 125
 Ile Tyr Ala Ala Cys Tyr Pro Glu Lys His Asn Glu Ser Lys Asn Phe
 130 135 140
 Ile Glu Asp Ile His His Leu Lys Thr Lys Val Asn Ala Gly Thr Asp
 145 150 155 160
 Lys Leu Ile Thr Gln Leu Phe Tyr Asp Asn Glu Asp Phe Tyr Thr Phe
 165 170 175
 Lys Gln Asn Cys Ala Leu Ala Asp Ile Asp Ile Pro Ile Tyr Ala Gly
 180 185 190
 Ile Met Pro Ile Thr Asn Lys Arg Gln Val Leu Lys Ile Ser Gln Leu
 195 200 205
 Cys Gly Ala Lys Ile Pro Pro Lys Phe Val Lys Ile Leu Glu Lys Tyr
 210 215 220
 Glu Asn Asn Thr Leu Ala Leu Glu Asp Ala Gly Ile Ala Tyr Ala Cys
 225 230 235 240
 Asp Gln Ile Val Asp Leu Ile Thr Ser Gly Val Asp Gly Ile His Leu
 245 250 255
 Tyr Thr Met Asn Lys Ser Lys Ala Ala Ile Lys Ile Tyr Glu Ala Val
 260 265 270
 Lys His Leu Leu Lys Glu Glu Leu His Ala
 275 280

<210> 49

<211> 852

<212> DNA

<213> Lactococcus lactis

<220>

<221> CDS

<222> (1)..(849)

<223> AAK05352

<400> 49

atg aca agt aat tcc aaa att ctt tct ttt gaa gtt ttt cca cct aca	48
Met Thr Ser Asn Ser Lys Ile Leu Ser Phe Glu Val Phe Pro Pro Thr	
1 5 10 15	
act caa att gga agt acc aac ttg gta aag acc ttg gat agc cta aga	96
Thr Gln Ile Gly Ser Thr Asn Leu Val Lys Thr Leu Asp Ser Leu Arg	
20 25 30	
act ctc tcg cca gat ttt atc agt gta act tgt agt aac aat aat tat	144
Thr Leu Ser Pro Asp Phe Ile Ser Val Thr Cys Ser Asn Asn Asn Tyr	
35 40 45	
gat aat att gga gat aca act ata aag ttt gct gat tat gta aac aat	192
Asp Asn Ile Gly Asp Thr Thr Ile Lys Phe Ala Asp Tyr Val Asn Asn	
50 55 60	
aca cta gat att cca gcg gtt gct cat tta cct gcc gct tat tta gat	240
Thr Leu Asp Ile Pro Ala Val Ala His Leu Pro Ala Ala Tyr Leu Asp	
65 70 75 80	
aaa gct caa gtg atc gaa att ttg gaa cgg tta aaa gat aaa caa atc	288
Lys Ala Gln Val Ile Glu Ile Leu Glu Arg Leu Lys Asp Lys Gln Ile	
85 90 95	
aaa aaa att ctt gct tta aga ggt gat atc agc gat gaa ccg atg aaa	336
Lys Lys Ile Leu Ala Leu Arg Gly Asp Ile Ser Asp Glu Pro Met Lys	
100 105 110	
gat gat ttt aaa ttt gca agt gat ttg gtt aaa ttt atc aaa gat tat	384
Asp Asp Phe Lys Phe Ala Ser Asp Leu Val Lys Phe Ile Lys Asp Tyr	
115 120 125	
gat gat agt ttt gaa gtt tta ggt gct tgc tac ccc gat att cat ccc	432
Asp Asp Ser Phe Glu Val Leu Gly Ala Cys Tyr Pro Asp Ile His Pro	
130 135 140	
gaa tca gta aat cga gtg agt gat ttt cat tat ctg aaa gaa aaa gta	480
Glu Ser Val Asn Arg Val Ser Asp Phe His Tyr Leu Lys Glu Lys Val	
145 150 155 160	
gat gct ggt tgt gac aga tta atc acg caa cta ttt ttt gat aat gat	528
Asp Ala Gly Cys Asp Arg Leu Ile Thr Gln Leu Phe Phe Asp Asn Asp	
165 170 175	
agt ttc tat gat ttt caa gaa cga tgc gca att gct gag ata aat act	576
Ser Phe Tyr Asp Phe Gln Glu Arg Cys Ala Ile Ala Glu Ile Asn Thr	
180 185 190	
ccg ata ttc gcc gga ata atg cca gta atc aat cga aat caa att ctt	624
Pro Ile Phe Ala Gly Ile Met Pro Val Ile Asn Arg Asn Gln Ile Leu	
195 200 205	
cgt cta tta aaa aat tgt aat acg cca tta cca gca aaa ttc att aga	672
Arg Leu Leu Lys Asn Cys Asn Thr Pro Leu Pro Ala Lys Phe Ile Arg	
210 215 220	
ata ctc gaa aaa tat gaa cat aat ctt atc gct tta agg gat gct gga	720

Ile Leu Glu Lys Tyr Glu His Asn Leu Ile Ala Leu Arg Asp Ala Gly
 225 230 235 240

att gct tac gcc atc gat caa atc gtt gat tta gta aca gag gat gtt 768
 Ile Ala Tyr Ala Ile Asp Gln Ile Val Asp Leu Val Thr Glu Asp Val
 245 250 255

gct gga att cac ctc tat acg atg aat aat gca aat acg gca cac tcc 816
 Ala Gly Ile His Leu Tyr Thr Met Asn Asn Ala Asn Thr Ala His Ser
 260 265 270

atc cat gct tca att tct tct tta ttt acc ttt tga 852
 Ile His Ala Ser Ile Ser Ser Leu Phe Thr Phe
 275 280

<210> 50

<211> 283

<212> PRT

<213> Lactococcus lactis

<400> 50

Met Thr Ser Asn Ser Lys Ile Leu Ser Phe Glu Val Phe Pro Pro Thr
 1 5 10 15

Thr Gln Ile Gly Ser Thr Asn Leu Val Lys Thr Leu Asp Ser Leu Arg
 20 25 30

Thr Leu Ser Pro Asp Phe Ile Ser Val Thr Cys Ser Asn Asn Asn Tyr
 35 40 45

Asp Asn Ile Gly Asp Thr Thr Ile Lys Phe Ala Asp Tyr Val Asn Asn
 50 55 60

Thr Leu Asp Ile Pro Ala Val Ala His Leu Pro Ala Ala Tyr Leu Asp
 65 70 75 80

Lys Ala Gln Val Ile Glu Ile Leu Glu Arg Leu Lys Asp Lys Gln Ile
 85 90 95

Lys Lys Ile Leu Ala Leu Arg Gly Asp Ile Ser Asp Glu Pro Met Lys
 100 105 110

Asp Asp Phe Lys Phe Ala Ser Asp Leu Val Lys Phe Ile Lys Asp Tyr
 115 120 125

Asp Asp Ser Phe Glu Val Leu Gly Ala Cys Tyr Pro Asp Ile His Pro
 130 135 140

Glu Ser Val Asn Arg Val Ser Asp Phe His Tyr Leu Lys Glu Lys Val
 145 150 155 160

Asp Ala Gly Cys Asp Arg Leu Ile Thr Gln Leu Phe Phe Asp Asn Asp
 165 170 175

Ser Phe Tyr Asp Phe Gln Glu Arg Cys Ala Ile Ala Glu Ile Asn Thr
 180 185 190

Pro Ile Phe Ala Gly Ile Met Pro Val Ile Asn Arg Asn Gln Ile Leu

195	200	205
Arg Leu Leu Lys Asn Cys Asn Thr Pro Leu Pro Ala Lys Phe Ile Arg		
210	215	220
Ile Leu Glu Lys Tyr Glu His Asn Leu Ile Ala Leu Arg Asp Ala Gly		
225	230	235
Ile Ala Tyr Ala Ile Asp Gln Ile Val Asp Leu Val Thr Glu Asp Val		
	245	250
Ala Gly Ile His Leu Tyr Thr Met Asn Asn Ala Asn Thr Ala His Ser		
	260	265
Ile His Ala Ser Ile Ser Ser Leu Phe Thr Phe		
275	280	

<210> 51
 <211> 891
 <212> DNA
 <213> Prochlorococcus maritima

<220>
 <221> CDS
 <222> (1)..(888)
 <223> RCK01602

<400> 51

ttg aaa tca aaa ctt cag caa act tta gaa aag aat tca aaa gta att	48
Leu Lys Ser Lys Leu Gln Gln Thr Leu Glu Lys Asn Ser Lys Val Ile	
1 5 10 15	
aca gca gaa tta atg ccg cca aga gga gga gac ccc gta aga tct ctt	96
Thr Ala Glu Leu Met Pro Pro Arg Gly Gly Asp Pro Val Arg Ser Leu	
20 25 30	
aaa ata gca caa ctc ttg aga aat aag gtg cat gca gtt aat att aca	144
Lys Ile Ala Gln Leu Leu Arg Asn Lys Val His Ala Val Asn Ile Thr	
35 40 45	
gac gga agt aga gca ata atg aga atg tgt agt tta gca atg tct aaa	192
Asp Gly Ser Arg Ala Ile Met Arg Met Cys Ser Leu Ala Met Ser Lys	
50 55 60	
cta tta cta gac aat ggg ata gaa cct ata atg cag atc tca tgt aga	240
Leu Leu Leu Asp Asn Gly Ile Glu Pro Ile Met Gln Ile Ser Cys Arg	
65 70 75 80	
gat cgt aat aaa att gct tta caa tca gat att ctt gga gca aat gcc	288
Asp Arg Asn Lys Ile Ala Leu Gln Ser Asp Ile Leu Gly Ala Asn Ala	
85 90 95	
tta gga att aaa aat att tta tgc att aca gga gat tct gta aaa gcc	336
Leu Gly Ile Lys Asn Ile Leu Cys Ile Thr Gly Asp Ser Val Lys Ala	
100 105 110	
gga gat cag caa gaa aca aaa gcc gtt cat gaa ttt gag gca gta aga	384
Gly Asp Gln Gln Glu Thr Lys Ala Val His Glu Phe Glu Ala Val Arg	
115 120 125	

tta tta aaa caa att caa tca ttc aat caa gga att gat cct act ttt 432
 Leu Leu Lys Gln Ile Gln Ser Phe Asn Gln Gly Ile Asp Pro Thr Phe
 130 135 140

gaa caa ctt cca gac aaa agg act gaa att ttc tca ggt gcg gca gta 480
 Glu Gln Leu Pro Asp Lys Arg Thr Glu Ile Phe Ser Gly Ala Ala Val
 145 150 155 160

gat cca agt tgt cga aat caa aga agt tta aaa agt aga aca att aaa 528
 Asp Pro Ser Cys Arg Asn Gln Arg Ser Leu Lys Ser Arg Thr Ile Lys
 165 170 175

aaa aaa gag gcc ggt gca aat ttc tta caa act caa ata gtt atg gat 576
 Lys Lys Glu Ala Gly Ala Asn Phe Leu Gln Thr Gln Ile Val Met Asp
 180 185 190

aga aaa tgt tta gca gac ttt tgc aac gaa atc agt aat cca ctt gag 624
 Arg Lys Cys Leu Ala Asp Phe Cys Asn Glu Ile Ser Asn Pro Leu Glu
 195 200 205

ata cca gtt att gca gga gta ttt ctt tta aaa tca tat aaa aat gct 672
 Ile Pro Val Ile Ala Gly Val Phe Leu Leu Lys Ser Tyr Lys Asn Ala
 210 215 220

ctt ttc ata aat aaa ttt gta cct gga gcg aat att cct gaa aat gtt 720
 Leu Phe Ile Asn Lys Phe Val Pro Gly Ala Asn Ile Pro Glu Asn Val
 225 230 235 240

tta aat cgt ctc aaa gat gca aaa aat cca ctt caa gaa gga ata tta 768
 Leu Asn Arg Leu Lys Asp Ala Lys Asn Pro Leu Gln Glu Gly Ile Leu
 245 250 255

att gct tca gag caa gct caa gat ttt att aat att gca gat gga att 816
 Ile Ala Ser Glu Gln Ala Gln Asp Phe Ile Asn Ile Ala Asp Gly Ile
 260 265 270

cat ctt atg gca gtc aaa tca gaa cat ctt atc cca gag ata ctt gaa 864
 His Leu Met Ala Val Lys Ser Glu His Leu Ile Pro Glu Ile Leu Glu
 275 280 285

aaa gct ggt ctc aat ctg gaa tgt taa 891
 Lys Ala Gly Leu Asn Leu Glu Cys
 290 295

<210> 52

<211> 296

<212> PRT

<213> *Prochlorococcus maritima*

<400> 52

Leu Lys Ser Lys Leu Gln Gln Thr Leu Glu Lys Asn Ser Lys Val Ile
 1 5 10 15

Thr Ala Glu Leu Met Pro Pro Arg Gly Gly Asp Pro Val Arg Ser Leu
 20 25 30

Lys Ile Ala Gln Leu Leu Arg Asn Lys Val His Ala Val Asn Ile Thr
 35 40 45

Asp Gly Ser Arg Ala Ile Met Arg Met Cys Ser Leu Ala Met Ser Lys
 50 55 60
 Leu Leu Leu Asp Asn Gly Ile Glu Pro Ile Met Gln Ile Ser Cys Arg
 65 70 75 80
 Asp Arg Asn Lys Ile Ala Leu Gln Ser Asp Ile Leu Gly Ala Asn Ala
 85 90 95
 Leu Gly Ile Lys Asn Ile Leu Cys Ile Thr Gly Asp Ser Val Lys Ala
 100 105 110
 Gly Asp Gln Gln Glu Thr Lys Ala Val His Glu Phe Glu Ala Val Arg
 115 120 125
 Leu Leu Lys Gln Ile Gln Ser Phe Asn Gln Gly Ile Asp Pro Thr Phe
 130 135 140
 Glu Gln Leu Pro Asp Lys Arg Thr Glu Ile Phe Ser Gly Ala Ala Val
 145 150 155 160
 Asp Pro Ser Cys Arg Asn Gln Arg Ser Leu Lys Ser Arg Thr Ile Lys
 165 170 175
 Lys Lys Glu Ala Gly Ala Asn Phe Leu Gln Thr Gln Ile Val Met Asp
 180 185 190
 Arg Lys Cys Leu Ala Asp Phe Cys Asn Glu Ile Ser Asn Pro Leu Glu
 195 200 205
 Ile Pro Val Ile Ala Gly Val Phe Leu Leu Lys Ser Tyr Lys Asn Ala
 210 215 220
 Leu Phe Ile Asn Lys Phe Val Pro Gly Ala Asn Ile Pro Glu Asn Val
 225 230 235 240
 Leu Asn Arg Leu Lys Asp Ala Lys Asn Pro Leu Gln Glu Gly Ile Leu
 245 250 255
 Ile Ala Ser Glu Gln Ala Gln Asp Phe Ile Asn Ile Ala Asp Gly Ile
 260 265 270
 His Leu Met Ala Val Lys Ser Glu His Leu Ile Pro Glu Ile Leu Glu
 275 280 285
 Lys Ala Gly Leu Asn Leu Glu Cys
 290 295

<210> 53

<211> 1848

<212> DNA

<213> *Bacillus stearothermophilus*

<220>

<221> CDS

<222> (1) .. (1845)

<223> RBE04103

<400> 53

gtg gga ttg ctg gat gag ttg aaa gag cgc att ctc atc gcc gac ggg	48
Val Gly Leu Leu Asp Glu Leu Lys Glu Arg Ile Leu Ile Ala Asp Gly	
1 5 10 15	
gcg atg gga acg ctt tta tat tgc cac ggc att gac cgt tgt ttt gaa	96
Ala Met Gly Thr Leu Leu Tyr Ser His Gly Ile Asp Arg Cys Phe Glu	
20 25 30	
gaa ttg aat cta tcc aat cca gat gaa atc gtc cat att cat gaa gcg	144
Glu Leu Asn Leu Ser Asn Pro Asp Glu Ile Val His Ile His Glu Ala	
35 40 45	
tat atc gcc gcg ggc gcc gac gtc att cag acg aat aca tac ggc gcc	192
Tyr Ile Ala Ala Gly Ala Asp Val Ile Gln Thr Asn Thr Tyr Gly Ala	
50 55 60	
aac tat gtg aaa ctc gcc cgc tac ggc ctt gaa gat gag gtg ccg gcc	240
Asn Tyr Val Lys Leu Ala Arg Tyr Gly Leu Glu Asp Glu Val Pro Ala	
65 70 75 80	
atc aac cgc gcg gcg gtg cgg ctc gcc agg caa gcg gcg aac gga cgg	288
Ile Asn Arg Ala Ala Val Arg Leu Ala Arg Gln Ala Ala Asn Gly Arg	
85 90 95	
gca tac gtg ctc ggg acg atc ggg ggg ctg cgc acg tta aac aaa agc	336
Ala Tyr Val Leu Gly Thr Ile Gly Gly Leu Arg Thr Leu Asn Lys Ser	
100 105 110	
gtc gtc acg ctc gaa gaa gtg aag cgg acg ttt cgc gag cag ctg ttt	384
Val Val Thr Leu Glu Glu Val Lys Arg Thr Phe Arg Glu Gln Leu Phe	
115 120 125	
gtc ctg ctc gct gaa ggg gtc gac ggc gtg ctg ctc gag acg tat tac	432
Val Leu Leu Ala Glu Gly Val Asp Gly Val Leu Leu Glu Thr Tyr Tyr	
130 135 140	
gat ttg gaa gag ttg gag acg gtg ctt gcc atc gcc cgc aaa gag acc	480
Asp Leu Glu Glu Leu Glu Thr Val Leu Ala Ile Ala Arg Lys Glu Thr	
145 150 155 160	
gac ttg ccg att atc gct cac gtc tgc ctc cat gaa gtc ggc gtc ttg	528
Asp Leu Pro Ile Ile Ala His Val Ser Leu His Glu Val Gly Val Leu	
165 170 175	
caa gat ggc acg ccg ctc gcg gac gcc ctt gcc cgc cta gag gcg ctc	576
Gln Asp Gly Thr Pro Leu Ala Asp Ala Leu Ala Arg Leu Glu Ala Leu	
180 185 190	
ggg gcc gat gtc gtc gga ctg aac tgt cgt ctc ggt cca tat cat atg	624
Gly Ala Asp Val Val Gly Leu Asn Cys Arg Leu Gly Pro Tyr His Met	
195 200 205	
ctt cgg tgc ctc gag gaa gtg ccg ctg cca aat cga gcg ttt ttg tgc	672
Leu Arg Ser Leu Glu Glu Val Pro Leu Pro Asn Arg Ala Phe Leu Ser	
210 215 220	
gcg tat ccg aac gcc agc ctt ccg gat tac cgc gat ggg ccg ctt gtc	720
Ala Tyr Pro Asn Ala Ser Leu Pro Asp Tyr Arg Asp Gly Arg Leu Val	

225	230	235	240	
tat gag acg aac gct gaa tat ttc gag gaa acg gcc aaa gcg ttc cgc				768
Tyr Glu Thr Asn Ala Glu Tyr Phe Glu Glu Thr Ala Lys Ala Phe Arg				
245		250	255	
gac caa ggg gtg cgc ttg atc ggc ggg tgc tgc ggc acg acg ccg aaa				816
Asp Gln Gly Val Arg Leu Ile Gly Gly Cys Cys Gly Thr Thr Pro Lys				
260		265	270	
cat atc gaa gcg atg gca aaa gcg ctc tcc gac cga acg ccg gtg acg				864
His Ile Glu Ala Met Ala Lys Ala Leu Ser Asp Arg Thr Pro Val Thr				
275		280	285	
gaa aaa acg gtg aaa cgg cgc gcg gtg tct gta tca gtg caa gcg gag				912
Glu Lys Thr Val Lys Arg Arg Ala Val Ser Val Ser Val Gln Ala Glu				
290		295	300	
cgg ccc gcc cca tct ccc ctt ccc gag ctt gcc cgc acg cac cgc tcg				960
Arg Pro Ala Pro Ser Pro Leu Pro Glu Leu Ala Arg Thr His Arg Ser				
305		310	315	320
gtc att gtg gag ctg gat ccg ccg aaa aaa ttg ggg att gac aag ttt				1008
Val Ile Val Glu Leu Asp Pro Pro Lys Lys Leu Gly Ile Asp Lys Phe				
325		330	335	
ctt gcc ggg gcg aaa gcg ctc cat gac gcc ggc atc gat gcg ctg acg				1056
Leu Ala Gly Ala Lys Ala Leu His Asp Ala Gly Ile Asp Ala Leu Thr				
340		345	350	
ttg gcc gac aac tcg ctc gcc acg ccg cgc atc agc aac gcc gct gtc				1104
Leu Ala Asp Asn Ser Leu Ala Thr Pro Arg Ile Ser Asn Ala Ala Val				
355		360	365	
gcc acg atc atc aag gag caa ctc ggc atc cgc ccg ctc gtg cat att				1152
Ala Thr Ile Ile Lys Glu Gln Leu Gly Ile Arg Pro Leu Val His Ile				
370		375	380	
aca tgc cgc gat cgc aat ttg atc ggc ttg cag tcg cat ttg atg ggc				1200
Thr Cys Arg Asp Arg Asn Leu Ile Gly Leu Gln Ser His Leu Met Gly				
385		390	395	400
ttg cat acg ctc ggc atc acc gat gtg ctc gcc att acc ggc gac ccg				1248
Leu His Thr Leu Gly Ile Thr Asp Val Leu Ala Ile Thr Gly Asp Pro				
405		410	415	
tcg aaa atc ggc gat ttt cca ggg gca acg tcc gtg tac gac tta tca				1296
Ser Lys Ile Gly Asp Phe Pro Gly Ala Thr Ser Val Tyr Asp Leu Ser				
420		425	430	
tcg ttc gat ttg atc cgc ttg atc cgc cag ttt aac gaa ggg ctg tcg				1344
Ser Phe Asp Leu Ile Arg Leu Ile Arg Gln Phe Asn Glu Gly Leu Ser				
435		440	445	
tac tcg ggc aaa ccg ctt ggg caa aaa acg aac ttc tcg atc ggc gct				1392
Tyr Ser Gly Lys Pro Leu Gly Gln Lys Thr Asn Phe Ser Ile Gly Ala				
450		455	460	
gcg ttc aac ccg aac gtc cgc cat ttg gac aaa gcg gtc gag ccg atg				1440
Ala Phe Asn Pro Asn Val Arg His Leu Asp Lys Ala Val Glu Arg Met				

465	470	475	480	
gag aaa aaa atc caa tgc ggc gcc cat tat ttc ttg acc cag ccg att				1488
Glu Lys Lys Ile Gln Cys Gly Ala His Tyr Phe Leu Thr Gln Pro Ile				
	485	490	495	
tac tcg gaa gag aaa atc gtt gaa gtg cac gaa gcg acc aag cat ctt				1536
Tyr Ser Glu Glu Lys Ile Val Glu Val His Glu Ala Thr Lys His Leu				
	500	505	510	
gac acg ccg att tac atc ggc att atg ccg ctt gtg agc gcg cgc aac				1584
Asp Thr Pro Ile Tyr Ile Gly Ile Met Pro Leu Val Ser Ala Arg Asn				
	515	520	525	
gcc gac ttt ttg cat cat gaa gtg ccg ggc att acg ctc tct gac gag				1632
Ala Asp Phe Leu His His Glu Val Pro Gly Ile Thr Leu Ser Asp Glu				
	530	535	540	
att cgc gcc cgc atg gcc gcc tgc agc ggc gac ccg gtg caa gca gcc				1680
Ile Arg Ala Arg Met Ala Ala Cys Ser Gly Asp Pro Val Gln Ala Ala				
	545	550	555	560
aag gaa ggc atc gct atc gcc aaa tcg ctc att gac gct gcg ttt gat				1728
Lys Glu Gly Ile Ala Ile Ala Lys Ser Leu Ile Asp Ala Ala Phe Asp				
	565	570	575	
ttg ttt aac ggc att tat ttg atc acg ccg ttc ttg cgc tac gac atg				1776
Leu Phe Asn Gly Ile Tyr Leu Ile Thr Pro Phe Leu Arg Tyr Asp Met				
	580	585	590	
acg gtc gag ctt gtc cgc tac att cac gaa aaa gaa gcg gcc gcc aaa				1824
Thr Val Glu Leu Val Arg Tyr Ile His Glu Lys Glu Ala Ala Ala Lys				
	595	600	605	
gaa agg aag gtt gtt cat ggc taa				1848
Glu Arg Lys Val Val His Gly				
	610	615		

<210> 54

<211> 615

<212> PRT

<213> Bacillus stearothermophilus

<400> 54

Val Gly Leu Leu Asp Glu Leu Lys Glu Arg Ile Leu Ile Ala Asp Gly			
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Ala Met Gly Thr Leu Leu Tyr Ser His Gly Ile Asp Arg Cys Phe Glu			
20	25	30	

Glu Leu Asn Leu Ser Asn Pro Asp Glu Ile Val His Ile His Glu Ala			
35	40	45	

Tyr Ile Ala Ala Gly Ala Asp Val Ile Gln Thr Asn Thr Tyr Gly Ala			
50	55	60	

Asn Tyr Val Lys Leu Ala Arg Tyr Gly Leu Glu Asp Glu Val Pro Ala			
65	70	75	80

Ile	Asn	Arg	Ala	Ala	Val	Arg	Leu	Ala	Arg	Gln	Ala	Ala	Asn	Gly	Arg	85	90	95
Ala	Tyr	Val	Leu	Gly	Thr	Ile	Gly	Gly	Leu	Arg	Thr	Leu	Asn	Lys	Ser	100	105	110
Val	Val	Thr	Leu	Glu	Glu	Val	Lys	Arg	Thr	Phe	Arg	Glu	Gln	Leu	Phe	115	120	125
Val	Leu	Leu	Ala	Glu	Gly	Val	Asp	Gly	Val	Leu	Leu	Glu	Thr	Tyr	Tyr	130	135	140
Asp	Leu	Glu	Glu	Leu	Glu	Thr	Val	Leu	Ala	Ile	Ala	Arg	Lys	Glu	Thr	145	150	155
Asp	Leu	Pro	Ile	Ile	Ala	His	Val	Ser	Leu	His	Glu	Val	Gly	Val	Leu	165	170	175
Gln	Asp	Gly	Thr	Pro	Leu	Ala	Asp	Ala	Leu	Ala	Arg	Leu	Glu	Ala	Leu	180	185	190
Gly	Ala	Asp	Val	Val	Gly	Leu	Asn	Cys	Arg	Leu	Gly	Pro	Tyr	His	Met	195	200	205
Leu	Arg	Ser	Leu	Glu	Glu	Val	Pro	Leu	Pro	Asn	Arg	Ala	Phe	Leu	Ser	210	215	220
Ala	Tyr	Pro	Asn	Ala	Ser	Leu	Pro	Asp	Tyr	Arg	Asp	Gly	Arg	Leu	Val	225	230	235
Tyr	Glu	Thr	Asn	Ala	Glu	Tyr	Phe	Glu	Glu	Thr	Ala	Lys	Ala	Phe	Arg	245	250	255
Asp	Gln	Gly	Val	Arg	Leu	Ile	Gly	Gly	Cys	Cys	Gly	Thr	Thr	Pro	Lys	260	265	270
His	Ile	Glu	Ala	Met	Ala	Lys	Ala	Leu	Ser	Asp	Arg	Thr	Pro	Val	Thr	275	280	285
Glu	Lys	Thr	Val	Lys	Arg	Arg	Ala	Val	Ser	Val	Ser	Val	Gln	Ala	Glu	290	295	300
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Val	Ile	Val	Glu	Leu	Asp	Pro	Pro	Lys	Lys	Leu	Gly	Ile	Asp	Lys	Phe	325	330	335
Leu	Ala	Gly	Ala	Lys	Ala	Leu	His	Asp	Ala	Gly	Ile	Asp	Ala	Leu	Thr	340	345	350
Leu	Ala	Asp	Asn	Ser	Leu	Ala	Thr	Pro	Arg	Ile	Ser	Asn	Ala	Ala	Val	355	360	365
Ala	Thr	Ile	Ile	Lys	Glu	Gln	Leu	Gly	Ile	Arg	Pro	Leu	Val	His	Ile	370	375	380
Thr	Cys	Arg	Asp	Arg	Asn	Leu	Ile	Gly	Leu	Gln	Ser	His	Leu	Met	Gly	385	390	395

Leu His Thr Leu Gly Ile Thr Asp Val Leu Ala Ile Thr Gly Asp Pro
 405 410 415

Ser Lys Ile Gly Asp Phe Pro Gly Ala Thr Ser Val Tyr Asp Leu Ser
 420 425 430

Ser Phe Asp Leu Ile Arg Leu Ile Arg Gln Phe Asn Glu Gly Leu Ser
 435 440 445

Tyr Ser Gly Lys Pro Leu Gly Gln Lys Thr Asn Phe Ser Ile Gly Ala
 450 455 460

Ala Phe Asn Pro Asn Val Arg His Leu Asp Lys Ala Val Glu Arg Met
 465 470 475 480

Glu Lys Lys Ile Gln Cys Gly Ala His Tyr Phe Leu Thr Gln Pro Ile
 485 490 495

Tyr Ser Glu Glu Lys Ile Val Glu Val His Glu Ala Thr Lys His Leu
 500 505 510

Asp Thr Pro Ile Tyr Ile Gly Ile Met Pro Leu Val Ser Ala Arg Asn
 515 520 525

Ala Asp Phe Leu His His Glu Val Pro Gly Ile Thr Leu Ser Asp Glu
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Ile Arg Ala Arg Met Ala Ala Cys Ser Gly Asp Pro Val Gln Ala Ala
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Lys Glu Gly Ile Ala Ile Ala Lys Ser Leu Ile Asp Ala Ala Phe Asp
 565 570 575

Leu Phe Asn Gly Ile Tyr Leu Ile Thr Pro Phe Leu Arg Tyr Asp Met
 580 585 590

Thr Val Glu Leu Val Arg Tyr Ile His Glu Lys Glu Ala Ala Ala Lys
 595 600 605

Glu Arg Lys Val Val His Gly
 610 615

<210> 55

<211> 52

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 55

cccggtatcc gctagcggcg cgccggccgg cccggtgtga aataccgcac ag

52

<210> 56

<211> 53

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 56

tctagactcg agcggccgcg gccggccttt aaattgaaga cgaaagggcc tcg 53

<210> 57

<211> 47

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 57

gagatctaga cccggggatc cgctagcggg ctgctaaagg aagcgga 47

<210> 58

<211> 38

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 58

gagaggcgcg ccgctagcgt gggcgaagaa ctccagca 38

<210> 59

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 59

gagagggcgg ccgcgcaaag tcccgttcg tgaa 34

<210> 60

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 60

gagagggcgg ccgctcaagt cggctcaagcc acgc 34

<210> 61

<211> 140

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 61

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tcgaatttaa atctcgagag gcctgacgtc gggcccggta ccacgcgtca tatgactagt 60
tcggacctag ggatatcgtc gacatcgatg ctcttctgcg ttaattaaca attgggatcc 120
tctagaccgc ggatttaaatt                                     140
```

<210> 62

<211> 140

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 62

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tgtcgacgat atccctaggc ccgaactagt catatgacgc gtggtaccgg gcccgacgct 120
aggcctctcg agatttaaatt                                     140
```

<210> 63

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 63

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gagagcggcc gccgacctt ttttaacctat cac                                     33
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<210> 64

<211> 32

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 64

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aggagcggcc gccatcggca ttttcttttg cg                                     32
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<210> 65

<211> 5091

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:plasmid

<400> 65

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accttatgc caagcttctt tcacctataa ttcgagagat tggattctta ccgtggaaat 120
tcttcgcaaa aatcgctccc tgatcgccct tgcgacgttg gcgtcggtgc cgctgggttg 180
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<210> 66

<211> 4323

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: plasmid

<400> 66

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ttcaaagagc tgtctgatgc tgatacgta acttgtagcag ttgtcagtg ttgtttgccg 180
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<210> 67

<211> 35

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR Primer

<400> 67

gagagagaga cgcggtcccag tggctgagac gcatc

35

<210> 68

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR Primer

<400> 68

ctctctctgt cgacgaattc aatcttacgg cctg

34

<210> 69

<211> 5860

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: plasmid

<400> 69

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aactgtcagc acgtagatcg aaaggtgcac aaaggtggcc ctggtcgtac agaaatatgg 180

cggttcctcg cttgagagtg cggaacgcat tagaaacgtc gctgaacgga tcgttgccac 240

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<210> 70

<211> 38

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR Primer

<400> 70

cggcaccacc gacatcatct tcacctgcc tcgttccg

38

<210> 71

<211> 38

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR Primer

<400> 71

cggaacgagg gcaggtgaag atgatgtcgg tgggtgccg

38

<210> 72

<211> 1266

<212> DNA

<213> LysC mutant

<220>

<221> CDS

<222> (1)..(1266)

<400> 72

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Val Ala Leu Val Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala
1 5 10 15

48

gaa cgc att aga aac gtc gct gaa cgg atc gtt gcc acc aag aag gct
Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala
20 25 30

96

gga aat gat gtc gtg gtt gtc tgc tcc gca atg gga gac acc acg gat
Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
35 40 45

144

gaa ctt cta gaa ctt gca gcg gca gtg aat ccc gtt ccg cca gct cgt Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg 50 55 60	192
gaa atg gat atg ctc ctg act gct ggt gag cgt att tct aac gct ctc Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu 65 70 75 80	240
gtc gcc atg gct att gag tcc ctt ggc gca gaa gcc caa tct ttc acg Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr 85 90 95	288
ggc tct cag gct ggt gtg ctc acc acc gag cgc cac gga aac gca cgc Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg 100 105 110	336
att gtt gat gtc act cca ggt cgt gtg cgt gaa gca ctc gat gag ggc Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly 115 120 125	384
aag atc tgc att gtt gct ggt ttc cag ggt gtt aat aaa gaa acc cgc Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg 130 135 140	432
gat gtc acc acg ttg ggt cgt ggt ggt tct gac acc act gca gtt gcg Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala 145 150 155 160	480
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ctg gaa aag ctc agc ttc gaa gaa atg ctg gaa ctt gct gct gtt ggc Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly 195 200 205	624
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tcc gat aag cca ggc gag gct gcg aag gtt ttc cgt gcg ttg gct gat Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp 275 280 285	864

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gac ggc acc acc gac atc atc ttc acc tgc cct cgt tcc gac ggc cgc	960
Asp Gly Thr Thr Asp Ile Ile Phe Thr Cys Pro Arg Ser Asp Gly Arg	
305 310 315 320	
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Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr	
325 330 335	
aat gtg ctt tac gac gac cag gtc ggc aaa gtc tcc ctc gtg ggt gct	1056
Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala	
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Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu	
355 360 365	
cgc gat gtc aac gtg aac atc gaa ttg att tcc acc tct gag att cgt	1152
Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg	
370 375 380	
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Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala	
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ttg cat gag cag ttc cag ctg ggc ggc gaa gac gaa gcc gtc gtt tat	1248
Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr	
405 410 415	
gca ggc acc gga cgc taa	1266
Ala Gly Thr Gly Arg	
420	

<210> 73

<211> 421

<212> PRT

<213> LysC mutant

<400> 73

Val Ala Leu Val Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala
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Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala
20 25 30

Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
35 40 45

Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg
 50 55 60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
 65 70 75 80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
 85 90 95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
 100 105 110

Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
 115 120 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
 130 135 140

Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala
 145 150 155 160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
 165 170 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
 180 185 190

Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
 195 200 205

Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
 210 215 220

Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
 225 230 235 240

Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
 245 250 255

Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile
 260 265 270

Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
 275 280 285

Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
290 295 300

Asp Gly Thr Thr Asp Ile Ile Phe Thr Cys Pro Arg Ser Asp Gly Arg
305 310 315 320

Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr
325 330 335

Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala
340 345 350

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
355 360 365

Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg
370 375 380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
385 390 395 400

Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr
405 410 415

Ala Gly Thr Gly Arg
420

<210> 74

<211> 5860

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: plasmid

<400> 74

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aactgtcagc acgtagatcg aaaggtgcac aaaggtggcc ctggtcgtac agaaatatgg      180
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<223> Description of the artificial sequence: PCR primer

<400> 75

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<213> Artificial sequence

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<223> Description of the artificial sequence: PCR primer

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<210> 77

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<213> Artificial sequence

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